

(19)



(11)

**EP 1 327 680 B1**

(12)

**EUROPEAN PATENT SPECIFICATION**

(45) Date of publication and mention  
of the grant of the patent:

**02.04.2008 Bulletin 2008/14**

(51) Int Cl.:

**C12N 15/09** (2006.01)

**C12N 15/62** (2006.01)

**C07K 16/28** (2006.01)

**A61K 39/395** (2006.01)

**C07K 16/24** (2006.01)

(21) Application number: **01978851.2**

(86) International application number:

**PCT/JP2001/009259**

(22) Date of filing: **22.10.2001**

(87) International publication number:

**WO 2002/033072 (25.04.2002 Gazette 2002/17)**

(54) **MODIFIED TPO AGONIST ANTIBODY**

MODIFIZIERTER TPO-AGONISTEN ANTIKÖRPER

ANTICORPS MODIFIE, AGONISTE DE TPO

(84) Designated Contracting States:

**AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU  
MC NL PT SE TR**

(30) Priority: **20.10.2000 JP 2000321821**

**17.04.2001 WOPCT/JP01/03288**

**12.09.2001 JP 2001277314**

(43) Date of publication of application:

**16.07.2003 Bulletin 2003/29**

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**Patent- und Rechtsanwälte**

**Arabellastrasse 4**

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(56) References cited:

**EP-A1- 1 035 132**

**WO-A-96/36360**

**WO-A-99/03495**

**WO-A-02/078612**

**WO-A1-00/53634**

**US-A- 5 885 574**

• **HUDSON P J ET AL: "High avidity scFv  
multimers; diabodies and triabodies" JOURNAL  
OF IMMUNOLOGICAL METHODS, ELSEVIER  
SCIENCE PUBLISHERS B.V., AMSTERDAM, NL,  
vol. 231, no. 1-2, 10 December 1999 (1999-12-10),  
pages 177-189, XP004187644 ISSN: 0022-1759**

• **BIJIA DENG ET AL.: 'An agonist murine  
monoclonal antibody to the human c-Mp1  
receptor stimulates megakaryocytopoiesis'  
BLOOD vol. 92, no. 6, 15 September 1998, pages  
1981 - 1988, XP002908248**

• **KIPRIYANOV ET AL.: 'Bispecific CD3XCD19  
diabody for T cell-mediated lysis of malignant  
human B cells' INT. J. CANCER vol. 77, no. 5, 1998,  
pages 763 - 772, XP002115487**

• **MING-HONG XIE ET AL.: 'Direct demonstration of  
MuSK involvement in acetylcholine receptor  
clustering through identification of agonist ScFv'  
NATURE BIOTECHNOLOGY vol. 15, no. 8, August  
1997, pages 768 - 771, XP002095742**

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**EP 1 327 680 B1**

**Description****TECHNICAL FIELD**

**[0001]** This invention relates to modified antibodies containing two or more H chain V regions and two or more L chain V regions of an antibody which show TPO agonist activity by crosslinking TPO receptor. The modified antibodies have TPO agonist activity of transducing a signal into cells by crosslinking TPO receptor and are useful as a medicine for various purposes.

**BACKGROUND ART**

**[0002]** Thrombopoietin (TPO) is a platelet production regulation factor found in 1994 and is known to be composed of a glycoprotein having a molecular weight of 70-80 thousands produced mainly in liver. Thrombopoietin is a cytokine which in bone marrow promotes platelet precursor cells to survive, proliferate, differentiate and mature, namely promotes megakaryocytes to differentiate and proliferate. Thrombopoietin (TPO) receptor was identified earlier than TPO as c-Mpl, a receptor of a specific factor to regulate platelet production (M. Souyri et al., Cell 63: 1137 (1990)). It was reported that c-Mpl is distributed mainly in platelet precursor cells, megakaryocytes and platelet cells and that the suppression of c-Mpl expression inhibits selectively megakaryocyte formation (M. Methia et al., Blood 82: 1395 (1993)). It was reported that the ligand to c-Mpl is TPO based on the results of proliferation assay of cells specific to c-Mpl ligand and purification of the ligand using c-Mpl (F. de Sauvage et al., Nature 369: 533 (1994); TD. Bartley et al., Cell 77: 1117 (1994)). At present Mpl is called TPO receptor. Therefore TPO and TPO receptor agonists have been expected to work as a therapeutic agent for thrombocytopenia, for example, as a medicine alleviating thrombocytopenia caused by bone marrow inhibition or bone marrow resection therapy for cancer patients.

**[0003]** On the other hand modified antibodies, especially antibodies with lowered molecular size, for example, single chain Fvs were developed to improve permeability into tissues and tumors by lowering molecular size and to produce by a recombinant method. Recently the dimers of single chain Fvs, especially bispecific-dimers have been used for crosslinking cells. Typical examples of such dimers are hetero-dimers of single chain Fvs recognizing antigens of cancer cells and antigens of host cells like NK cells and neutrophils (Kipriyanov et al., Int. J. Cancer, 77, 9763-9772, 1998). They were produced by construction technique of single chain Fv as modified antibodies, which are more effective in treating cancers by inducing intercellular crosslinking. It has been thought that the intercellular crosslinking is induced by antibodies and their fragments (e.g. Fab fragment), bispecific modified antibodies and even dimers of single chain Fvs, which are monospecific.

**[0004]** As antibodies capable of transducing a signal by crosslinking a cell surface molecule(s), there are known an antibody against EPO receptor involved in cell differentiation and proliferation (JP-A 2000-95800), an antibody against MuSK receptor (Xie et al., Nature Biotech. 15, 768-771, 1997) and others. There are also known an agonist antibody to TPO receptor, its fragments and single chain Fvs (WO99/10494). However there have been no reports on single chain Fv dimers and modified antibodies such as single chain bivalent antibodies having agonist activity.

**[0005]** Noticing that single chain Fv monomers derived from monoclonal antibodies (antibody MABL-1 and antibody MABL-2 produced by the inventors) which induce apoptosis of IAP-containing cells do not induce apoptosis of cells and that dimers induce apoptosis, the inventors discovered that dimers crosslink (dimerize) IAP receptor on cell surface, thereby a signal is transduced into the cells and, as a result, apoptosis is induced. This suggests that monospecific single chain Fv dimers crosslink a cell surface molecule (s) (e.g. receptor) and transduce a signal like a ligand, thereby serving as an agonist.

**[0006]** Focusing on the intercellular crosslinking, it was discovered that the above-mentioned single chain Fv dimers do not cause hemagglutination while the above-mentioned monoclonal antibodies do. The same result was also observed with single chain bivalent antibodies (single chain polypeptides containing two H chain V regions and two L chain V regions). This suggests that monoclonal antibodies may form intercellular crosslinking while modified antibodies like single chain Fv dimers and single chain bivalent antibodies crosslink a cell surface molecule(s) but do not form intercellular crosslinking.

**[0007]** Based on those observations the inventors have newly discovered that modified antibodies such as single chain Fv dimers and single chain bivalent antibodies crosslink a cell surface molecule(s) or intracellular molecule(s) of the same cell, in addition to known intercellular crosslinking, and are suitable as a ligand to the molecule(s) (especially as a ligand which mimics the action of natural ligand).

**[0008]** Discovering further that an antibody molecule (whole IgG) can be modified into single chain Fv dimers, single chain bivalent antibodies and the like which crosslink a cell surface molecule(s), thereby reducing side effects caused by intercellular crosslinking and providing new medicines inducing only desired effect on the cell, the inventors completed the invention. The modified antibodies of the invention have remarkably high activity compared with whole antibodies (IgG) having the same V region as the modified antibodies. They have an improved permeability into tissues due to the

lowered molecular size compared with antibody molecules and the lack of constant regions.

## DISCLOSURE OF INVENTION

**[0009]** An object of this invention is to provide low molecular-sized agonistic modified antibodies which contain two or more H chain V regions and two or more L chain V regions of a monoclonal antibody and have TPO agonist action by crosslinking TPO receptor.

**[0010]** Therefore, this invention relates the modified antibodies which contain two or more H chain V regions and two or more L chain V regions, preferably 2 to 6 each, especially preferably 2 to 4 each, most preferably two each, and show TPO agonist activity by crosslinking TPO receptor.

**[0011]** The "modified antibodies" in the specification mean any substances which contain two or more H chain V regions and two or more L chain V regions, wherein said V regions are combined directly or via linker through covalent bond or non-covalent bond. For example, polypeptides and compounds produced by combining each V region of antibody through a peptide linker or a chemical crosslinking agent and the like. Two or more H chain V regions and two or more L chain V regions used in the invention can be derived from the same antibody or from different antibodies.

**[0012]** Modified antibodies of the invention can be any things as long as they specifically recognize and crosslink TPO receptor and thereby can transduce a signal into cells. They include modified antibodies produced by further modifying a part of the amino acid sequence of V region of the modified antibodies.

**[0013]** Preferable examples of the modified antibodies of the invention are multimers such as dimers, trimers or tetramers of single chain Fv containing an H chain V region and an L chain V region, or single chain polypeptides containing two or more H chain V regions and two or more L chain V regions. When the modified antibodies of the invention are multimers of single chain Fv such as dimers, trimers, tetramers and the like containing an H chain V region and an L chain V region, it is preferable that the H chain V region and L chain V region existing in the same chain are not associated to form an antigen-binding site.

**[0014]** More preferable examples are dimers of the single chain Fv which contains an H chain V region and an L chain V region, or a single chain polypeptide containing two H chain V regions and two L chain V regions. The H chain V region and L chain V region are connected preferably through a linker in the modified antibodies.

**[0015]** The above-mentioned single chain Fv multimer includes a multimer by non-covalent bond, a multimer by a covalent bond through a crosslinking radical and a multimer through a crosslinking reagent (an antibody, an antibody fragment, or bivalent modified antibody). Conventional crosslinking radicals used for crosslinking peptides can be used as the crosslinking radicals to form the multimers. Examples are disulfide crosslinking by cysteine residue, other crosslinking radicals such as C<sub>4</sub> - C<sub>10</sub> alkylene (e.g. tetramethylene, pentamethylene, hexamethylene, heptamethylene and octamethylene, etc.) or C<sub>4</sub> - C<sub>10</sub> alkenylene (cis/trans -3-butenylene, cis/trans-2-pentenylene, cis/trans-3-pentenylene, cis/trans-3-hexenylene, etc.).

**[0016]** Moreover, the crosslinking reagent which can combine with a single chain Fv is, for example, an amino acid sequence which can optionally be introduced into Fv, for example, an antibody against FLAG sequence and the like or a fragment thereof, or a modified antibody originated from the antibody, for example, single chain Fv.

**[0017]** "TPO agonist action" in the specification means a biological action occurring in the cell(s) into which a signal is transduced by crosslinking TPO receptor, for example, proliferation, differentiation or growth stimulation of megakaryocytes, or platelet production.

**[0018]** ED50 of the TPO agonist action in the invention is determined by known methods for measuring agonist action. Examples for measurement are cell proliferation assay using TPO sensitive cell lines such as BaF/mp1 or UT7/TPO, measurement of phosphorylation of MPL protein, megakaryocyte colony assay by differentiation from bone marrow cells, in vivo mouse platelet recovery synthesis assay, measurement of expression induction of platelet antigen GPIIb/IIIa (anti GPIIb/IIIa) using human leukemia megakaryoblastic cell line (CMK) or measurement of polyploidy induction of megakaryoblastic cell line (DAMI). ED50 is a dose needed for achieving 50% reaction of the maximum activity set as 100%

**[0019]** in the dose-reaction curve.

**[0020]** Preferable modified antibodies of the invention have TPO agonist action (ED50) equivalent to or better than that of an antibody having the same antigen-binding region as the modified antibody, namely the whole antibody (hereinafter "parent antibody") like IgG having the same pair of H chain V region and L chain V region as the pair of H chain V region and L chain V region forming antigen-binding region of the modified antibody. More preferable are those having TPO agonist action (ED50) more than two times higher than that of parent antibody, further preferably more than 5 times, most preferably more than 10 times. The invention includes modified antibodies with TPO agonist action containing H chain V region and L chain V region forming the same antigen-binding region as the parent antibody which binds to TPO receptor but has no TPO agonist action to the molecule.

**[0021]** The compounds containing two or more H chain V regions and two or more L chain V regions of the invention can be any compounds which contain two or more H chain V regions and two or more L chain V regions of antibody and show TPO agonist action (ED50) equivalent to or better than that of thrombopoietin (TPO). Preferable are those

having TPO agonist action (ED50) more than two times higher than that of TPO, more preferably more than 5 times, most preferably more than 10 times.

**[0022]** The "compounds" mentioned here include not only modified antibodies of the invention but also any compounds containing two or more, preferably from 2 to 6, more preferably from 2 to 4, most preferably 2 antigen-binding regions such as whole antibodies or F(ab')<sub>2</sub>.

**[0023]** Preferable modified antibodies or compounds of the invention containing two or more H chain V regions and two or more L chain V regions of antibody have an intercellular adhesion action (ED50) not more than 1/10 compared with the parent antibody, more preferably have no substantial intercellular adhesion action.

**[0024]** ED50 of the intercellular adhesion action mentioned in the above is determined by known methods for measuring intercellular adhesion action, for example, by the measurement of agglomeration of cells expressing TPO receptor.

**[0025]** The invention relates to DNAs which code for the modified antibodies.

**[0026]** The invention relates to animal cells or microorganisms which produce the modified antibodies.

**[0027]** The invention relates to use of the modified antibody as TPO agonist.

**[0028]** The invention relates to a method of transducing a signal into cells by crosslinking TPO receptor using the modified antibody and thereby inducing TPO agonist action such as proliferation, differentiation-induction or growth stimulation of megakaryocytes, platelet production, phosphorylation of TPO receptor protein and the like.

**[0029]** The invention relates to a medicine for treating thrombocytopenia etc. containing the modified antibody as active component.

**[0030]** The invention relates to use of the modified antibody as a medicine.

**[0031]** The invention relates to a method of screening or measuring the modified antibody, which contains two or more H chain V regions and two or more L chain V regions of antibody and shows TPO agonist action by crosslinking TPO receptor, that comprises 1) to prepare a modified antibody containing two or more H chain V regions and two or more L chain V regions of antibody and binding specifically to TPO receptor, 2) to contact the modified antibody with cells expressing TPO receptor and 3) to measure TPO agonist action which occurs in the cells by crosslinking TPO receptor. The method of measurement is useful for the quality control in producing the modified antibodies of the invention as a medicine and other purposes.

**[0032]** The modified antibodies can be mono-specific modified antibodies or multi-specific modified antibodies like bi-specific modified antibodies. Preferable are mono-specific modified antibodies.

**[0033]** The present invention also relates to modified antibodies whose H chain V region and/or L chain V region is H chain V region derived from human antibody and/or L chain V region derived from human antibody. The H chain V region and/or L chain V region derived from human antibody can be obtained by screening human monoclonal antibody library as described in WO99/10494. The H chain V region and L chain V region derived from human monoclonal antibodies produced by transgenic mouse and the like are also included.

**[0034]** The present invention further relates to modified antibodies whose H chain V regions and/or L chain V regions are humanized H chain V regions and/or humanized L chain V regions. Specifically, the humanized modified antibodies consist of the humanized L chain V region which comprises framework regions (FR) derived from an L chain V region of human monoclonal antibody and complementarity determining regions (hereinafter "CDR") derived from an L chain V region of non-human mammalian (e.g. mouse, rat, bovine, sheep, ape) monoclonal antibody and/or the humanized H chain V region which comprises FR derived from an H chain V region of human monoclonal antibody and CDR derived from an H chain V region of non-human mammalian (e.g. mouse, rat, bovine, sheep, ape) monoclonal antibody. In this case, the amino acid sequences of CDR and FR may be partially altered, e.g. deleted, replaced or added.

**[0035]** H chain V regions and/or L chain V regions of the modified antibodies of the invention can be H chain V regions and/or L chain V regions derived from monoclonal antibodies of animals other than human (such as mouse, rat, bovine, sheep, ape, chicken and the like). In this case, the amino acid sequences of CDR and FR may be partially altered, e.g. deleted, replaced or added.

**[0036]** The invention also relates to DNAs encoding the various modified antibodies as mentioned above and genetic engineering techniques for producing recombinant vectors comprising the DNAs.

**[0037]** The invention also relates to host cells transformed with the recombinant vectors. Examples of host cells are animal cells such as human cells, mouse cells or the like and microorganisms such as *E. coli*, *Bacillus subtilis*, yeast or the like.

**[0038]** The invention relates to a process for producing the modified antibodies, which comprises culturing the above-mentioned hosts and extracting the modified antibodies from the culture thereof.

**[0039]** The present invention further relates to a process for producing a dimer of the single chain Fv which comprises culturing host animal cells producing the single chain Fv in a serum-free medium to secrete the single chain Fv into the medium and isolating the dimer of the single chain Fv formed in the medium.

**[0040]** The present invention also relates to the use of the modified antibodies as TPO agonist. That is, it relates to a signal-transduction agonist which comprises as an active ingredient the modified antibody obtained as mentioned in the above.

**[0041]** Therefore, the pharmaceutical preparations containing TPO agonist modified antibodies of the invention as an active ingredient are useful as preventives and/or remedies for platelet-reduction-related blood diseases, thrombocytopenia caused by chemotherapy of cancers or leukemia, and the like.

**[0042]** The modified antibodies of the present invention comprise two or more H chain V regions and two or more L chain V regions derived from antibodies. The structure of the modified antibodies may be a dimer of single chain Fv comprising one H chain V region and one L chain V region or a polypeptide comprising two H chain V regions and two L chain V regions. In the modified antibodies of the invention, the V regions of H chain and L chain are preferably linked through a peptide linker which consists of one or more amino acids. The resulting modified antibodies contain variable regions of antibodies and bind to the antigen with the same specificity as that of the original monoclonal antibodies.

H chain V region

**[0043]** In the present invention, the H chain V region derived from an antibody recognizes TPO receptor and oligomerizes, for example, dimerizes through crosslinking said molecule, and thereby transduces a signal into the cells. The H chain V region of the invention includes H chain V regions derived from a mammal (e.g. human, mouse, rat, bovine, sheep, ape etc.) and H chain V regions having partially modified amino acid sequences of the H chain V regions. More preferable is a humanized H chain V region containing FR of H chain V region of a human monoclonal antibody and CDR of H chain V region of a mouse monoclonal antibody. Also preferable is an H chain V region having an amino acid sequence derived from a human, which can be produced by recombination technique. The H chain V region of the invention may be a fragment of aforementioned H chain V region, which fragment preserves the antigen binding capacity.

L chain V region

**[0044]** In the present invention, the L chain V region recognizes TPO receptor and oligomerizes, for example, dimerizes through crosslinking said molecule, and thereby transduces a signal into the cells. The L chain V region of the invention includes L chain V regions derived from a mammal (e.g. human, mouse, rat, bovine, sheep, ape etc.) and L chain V regions having partially modified amino acid sequences of the L chain V regions. More preferable is a humanized L chain V region containing FR of L chain V region of human monoclonal antibody and CDR of L chain V region of mouse monoclonal antibodies. Also preferable is an L chain V region having an amino acid sequence derived from a human, which can be produced by recombination technique. The L chain V regions of the invention may be fragments of L chain V region, which fragments preserve the antigen binding capacity.

Complementarity determining region (CDR)

**[0045]** Each V region of L chain and H chain forms an antigen-binding site. The variable region of the L and H chains is composed of comparatively conserved four common framework regions linked to three hypervariable regions or complementarity determining regions (CDR) (Kabat, E.A. et al., "Sequences of Protein of Immunological Interest", US Dept. Health and Human Services, 1983).

**[0046]** Major portions in the four framework regions (FRs) form  $\beta$ -sheet structures and thus three CDRs form a loop. CDRs may form a part of the  $\beta$ -sheet structure in certain cases. The three CDRs are held sterically close position to each other by FR, which contributes to the formation of the antigen-binding site together with three CDRs.

**[0047]** These CDRs can be identified by comparing the amino acid sequence of V region of the obtained antibody with known amino acid sequences of V regions of known antibodies according to the empirical rule in Kabat, E.A. et al., "Sequences of Protein of Immunological Interest". Single chain Fv

**[0048]** A single chain Fv is a polypeptide monomer comprising an H chain V region and an L chain V region linked each other which are derived from antibodies. The resulting single chain Fvs contain variable regions of the original antibodies and preserve the complementarity determining region thereof, and therefore the single chain Fvs bind to the antigen by the same specificity as that of the original antibodies (JP-Appl. 11-63557). A part of the variable region and/or CDR of the single chain Fv of the invention or a part of the amino acid sequence thereof may be partially altered, for example, deleted, replaced or added. The H chain V region and L chain V region composing the single chain Fv of the invention are mentioned before and may be linked directly or through a linker, preferably a peptide linker. The constitution of the single chain Fv may be [H chain V region]-[L chain V region] or [L chain V region]-[H chain V region]. In the present invention, it is possible to make the single chain Fv to form a dimer, a trimer or a tetramer, from which the modified antibody of the invention can be formed.

Single chain modified antibody

**[0049]** The single chain modified antibodies of the present invention comprising two or more H chain V regions and

two or more L chain V regions, preferably each two to four, especially preferable each two, comprise two or more H chain V regions and L chain V regions as mentioned above. Each region of the peptide should be arranged such that the modified single chain antibody forms a specific steric structure, concretely mimicking a steric structure formed by the dimer of single chain Fv. For instance, the V regions are arranged in the order of the following manner:

[H chain V region]-[L chain V region]-[H chain V region]-[L chain V region]; or  
[L chain V region]-[H chain V region]-[L chain V region]-[H chain V region],

wherein these regions are connected through a peptide linker, respectively.

Linker

**[0050]** In this invention, the linkers for the connection between the H chain V region and the L chain V region may be any peptide linker which can be introduced by the genetic engineering procedure or any linker chemically synthesized. For instance, linkers disclosed in literatures, e.g. Protein Engineering, 9(3), 299-305, 1996 may be used in the invention. These linkers can be the same or different in the same molecule. If peptide linkers are required, the following are cited as example linkers:

Ser  
Gly-Ser  
Gly-Gly-Ser  
Ser-Gly-Gly  
Gly-Gly-Gly-Ser  
Ser-Gly-Gly-Gly  
Gly-Gly-Gly-Gly-Ser  
Ser-Gly-Gly-Gly-Gly  
Gly-Gly-Gly-Gly-Gly-Ser  
Ser-Gly-Gly-Gly-Gly-Gly  
Gly-Gly-Gly-Gly-Gly-Gly-Ser  
Ser-Gly-Gly-Gly-Gly-Gly-Gly  
(Gly-Gly-Gly-Gly-Ser)<sub>n</sub> and  
(Ser-Gly-Gly-Gly-Gly)<sub>n</sub>

wherein n is an integer not less than one. Preferable length of the linker peptide varies dependent upon the receptor to be the antigen, in the case of single chain Fvs, the range of 1 to 20 amino acids is normally preferable. In the case of single chain modified antibodies comprising two or more H chain V regions and two or more L chain V regions, the peptide linkers connecting those forming the same antigen binding site comprising [H chain V region]-[L chain V region] (or [L chain V region]-[H chain V region]) have lengths of 1 - 30 amino acids, preferably 1 - 20 amino acids, more preferably 3 - 18 amino acids. The peptide linkers connecting those not forming the same antigen binding site comprising [H chain V region]-[L chain V region] or ([L chain V region]-[H chain V region]) have lengths of 1 - 40 amino acids, preferably 3 - 30 amino acids, more preferably 5 - 20 amino acids. The method for introducing those linkers will be described in the explanation for DNA construction coding for modified antibodies of the invention.

**[0051]** The chemically synthesized linkers, i.e. the chemical crosslinking agents, according to the invention can be any linkers conventionally employed for the linkage of peptides. Examples of the linkers may include N-hydroxy succinimide (NHS), disuccinimidyl suberate (DSS), bis(sulfosuccinimidyl)suberate (BS<sup>3</sup>), dithiobis(succinimidyl propionate) (DSP), dithiobis(sulfosuccinimidyl propionate) (DTSSP), ethylene glycolbis(succinimidyl succinate) (EGS), ethylene glycolbis(sulfosuccinimidyl succinate) (sulfo-EGS), disuccinimidyl tartrate (DST), disulfosuccinimidyl tartrate (sulfo-DST), bis[2-(succinimido oxycarbonyloxy)ethyl]sulfone (BSOCOES), bis[2-(sulfosuccinimido oxycarbonyloxy)ethyl]sulfone (sulfo-BSOCOES) or the like. These are commercially available. It is preferable for the chemically synthesized linkers to have the length equivalent to that of peptide linkers.

**[0052]** To form a dimer of the single chain Fv it is preferable to select a linker suitable to dimerize in the solution such as culture medium more than 20%, preferably more than 50%, more preferably more than 80%, most preferably more than 90% of the single chain Fv produced in the host cells. Specifically, preferable is a linker composed of 2 to 12 amino acids, preferably 3 to 10 amino acids or other linkers corresponding thereto.

Preparation of modified antibodies

**[0053]** The modified antibodies can be produced by connecting, through the aforementioned linker, an H chain V

region and an L chain V region derived from known or novel antibodies specifically binding to TPO receptor. As examples of the single chain Fvs are cited those having H chain V region and L chain V region of antibody 12B5 and antibody 12E10 described in WO99/10494. As examples of the modified antibodies of the invention having two or more H chain V regions and two or more L chain V regions are cited sc12B5 dimer (linker: 15 amino acids), sc12E10 dimer (linker: 15 amino acids), db12B5 dimer (linker: 5 amino acids), db12E10 dimer (linker: 5 amino acids), sc12B5sc(FV)<sub>2</sub> and sc12E10sc (FV)<sub>2</sub> which contain H chain V regions and L chain V regions derived from the above-mentioned monoclonal antibodies.

**[0054]** For the preparation of the modified antibodies, a signal peptide may be attached to its N-terminal if the polypeptide is desired to be a secretory peptide. A well-known amino acid sequence useful for the purification of polypeptide such as the FLAG sequence may be attached for the efficient purification of the polypeptide. In this case a dimer can be formed by using anti-FLAG antibody.

**[0055]** For the preparation of the modified antibody of the invention, it is necessary to obtain a DNA, i.e. a DNA encoding the single chain Fv or a DNA encoding reconstructed single chain polypeptide. These DNAs, especially for sc12B5, db12B5, sc12E10 and/or db12E10 are obtainable from the DNAs encoding the H chain V regions and the L chain V regions derived from said Fvs. They are also obtainable by polymerase chain reaction (PCR) method using those DNAs as a template and amplifying the part of DNA contained therein encoding desired amino acid sequence with the aid of a pair of primers corresponding to both ends thereof.

**[0056]** In the case where each V region having partially modified amino acid sequence is desired, the V regions in which one or some amino acids are modified, i.e. deleted, replaced or added can be obtained by a procedure known in the art using PCR. A part of the amino acid sequence in the V region is preferably modified by the PCR known in the art in order to prepare the modified antibody which is sufficiently active against the specific antigen.

**[0057]** For the determination of primers for the PCR amplification, the types of H chain and L chain, if a monoclonal antibody is used as a starting material, are determined by a typing method known in the technical field.

**[0058]** For the amplification of the L chain V regions of antibody 12B5 and antibody 12E10 by PCR, 5'-end and 3'-end oligonucleotide primers are decided as aforementioned. In the same manner, 5'-end and 3'-end oligonucleotide primers are decided for the amplification of the H chain V regions of antibody 12B5 and antibody 12E10.

**[0059]** In embodiments of the invention, the 5'-end primers which contain a sequence "GATC" providing the restriction enzyme Hinf I recognition site at the neighborhood of 5'-terminal thereof are used and the 3'-end primers which contain a nucleotide sequence "CCCGGG" providing the XmaI recognition site at the neighborhood of 5'-terminal thereof are used. Other restriction enzyme recognition site may be used instead of these sites as long as they are used for subcloning a desired DNA fragment into a cloning vector.

**[0060]** Specifically designed PCR primers are employed to provide suitable nucleotide sequences at 5'-end and 3'-end of the cDNAs encoding the V regions of the antibodies 12B5 and 12E10 so that the cDNAs are readily inserted into an expression vector and appropriately function in the expression vector (e.g. this invention devises to increase transcription efficiency by inserting Kozak sequence). The V regions of the antibodies 12B5 and 12E10 obtained by amplifying by PCR using these primers are inserted into HEF expression vector containing the desired human C region (see WO92/19759). The cloned DNAs can be sequenced by using any conventional process, for example, by the automatic DNA sequencer (Applied Biosystems).

**[0061]** A linker such as a peptide linker can be introduced into the modified antibody of the invention in the following manner. Primers which have partially complementary sequence with the primers for the H chain V regions and the L chain V regions as described above and which code for the N-terminal or the C-terminal of the linker are designed. Then, the PCR procedure can be carried out using these primers to prepare a DNA encoding the peptide linker having desired amino acid sequence and length. The DNAs encoding the H chain V region and the L chain V region can be connected through the resulting DNA to produce the DNA encoding the modified antibody of the invention which has the desired peptide linker. Once the DNA encoding one of the modified antibodies is prepared, the DNAs encoding the modified antibodies with or without the desired peptide linker can readily be produced by designing various primers for the linker and then carrying out the PCR using the primers and the aforementioned DNA as a template.

**[0062]** Each V region of the modified antibody of the present invention can be humanized by using conventional techniques (e.g. Sato, K. et al., Cancer Res., 53, 1-6 (1993)). Once a DNA encoding each of humanized Fvs is prepared, a humanized single chain Fv, a fragment of the humanized single chain Fv, a humanized monoclonal antibody and a fragment of the humanized monoclonal antibody can readily be produced according to conventional methods. Preferably, amino acid sequences of the V regions thereof may be partially modified, if necessary.

**[0063]** Furthermore, a DNA derived from other mammalian origin, for example a DNA encoding each of V regions of human antibody, can be produced in the same manner as used to produce DNA encoding the H chain V region and the L chain V region derived from mouse by conventional methods as mentioned in the above. The resulting DNA can be used to prepare an H chain V region and an L chain V region of other mammal, especially derived from human antibody, a single chain Fv derived from human and a fragment thereof, and a monoclonal antibody of human origin and a fragment thereof.

**[0064]** When the modified antibodies of the invention is bi-specific modified antibodies, they can be produced by known methods (for example, the method described in WO9413804).

**[0065]** As mentioned above, when the aimed DNAs encoding the V regions of the modified antibodies and the V regions of the humanized modified antibodies are prepared, the expression vectors containing them and hosts transformed with the vectors can be obtained according to conventional methods. Further, the hosts can be cultured according to a conventional method to produce the reconstructed single chain Fv, the reconstructed humanized single chain Fv, the humanized monoclonal antibodies and fragments thereof. They can be isolated from cells or a medium and can be purified into a homogeneous mass. For this purpose any isolation and purification methods conventionally used for proteins, e.g. chromatography, ultra-filtration, salting-out and dialysis, may be employed in combination, if necessary, without limitation thereto..

**[0066]** When the reconstructed single chain Fv of the present invention is produced by culturing an animal cell such as COS7 cells or CHO cells, preferably CHO cells, in a serum-free medium, the dimer of said single chain Fv formed in the medium can be stably recovered and purified in a high yield. Thus purified dimer can be stably preserved for a long period. The serum-free medium employed in the invention may be any medium conventionally used for the production of a recombinant protein without limit thereto.

**[0067]** For the production of the modified antibodies of the present invention, any expression systems can be employed, for example, eukaryotic cells such as animal cells, e.g., established mammalian cell lines, filamentous fungi and yeast, and prokaryotic cells such as bacterial cells e.g., *E. coli*. Preferably, the modified antibodies of the invention are expressed in mammalian cells, for example COS7 cells or CHO cells.

**[0068]** In these cases, conventional promoters useful for the expression in mammalian cells can be used. Preferably, human cytomegalovirus (HCMV) immediate early promoter is used. Expression vectors containing the HCMV promoter include HCMV-VH-HC $\gamma$  1, HCMV-VL-HCK and the like which are derived from pSV2neo (WO92/19759).

**[0069]** Additionally, other promoters for gene expression in mammal cell which may be used in the invention include virus promoters derived from retrovirus, polyoma virus, adenovirus and simian virus 40 (SV40) and promoters derived from mammal such as human polypeptide-chain elongation factor-1 $\alpha$  (HEF-1 $\alpha$ ). SV40 promoter can easily be used according to the method of Mulligan, R.C., et al. (Nature 277, 108-114 (1979)) and HEF-1 $\alpha$  promoter can also be used according to the methods of Mizushima, S. et al. (Nucleic Acids Research, 18, 5322 (1990)).

**[0070]** Replication origin (ori) which can be used in the invention includes ori derived from SV40, polyoma virus, adenovirus, bovine papilloma virus (BPV) and the like. An expression vector may contain, as a selection marker, phosphotransferase AHP (3') II or I (neo) gene, thymidine kinase (TK) gene, *E. coli* xanthine-guanine phosphoribosyl transferase (Ecogpt) gene or dihydrofolate reductase (DHFR) gene.

**[0071]** The antigen-binding activity of the modified antibody prepared in the above can be evaluated by a conventional method such as radio immunoassay (RIA), enzyme-linked immunosorbent assay (ELISA) or surface plasmon resonance. It can also be evaluated using the binding-inhibitory ability of original antibody as an index, for example in terms of the absence or presence of concentration-dependent inhibition of the binding of said monoclonal antibody to the antigen.

**[0072]** More in detail, animal cells transformed with an expression vector containing a DNA encoding the modified antibody of the invention, e.g., COS7 cells or CHO cells, are cultured. The cultured cells and/or the supernatant of the medium or the modified antibody purified from them are used to determine the binding to antigen. As a control is used a supernatant of the culture medium in which cells transformed only with the expression vector were cultured. In the case of an antigen, for example, the antibody 1285 and the antibody 12E10, a test sample of the modified antibody of the invention or a supernatant of the control is added to Ba/F3 cells expressing human MPL and then an assay such as the flow cytometry is carried out to evaluate the antigen-binding activity.

**[0073]** In vitro evaluation of the signal transduction effect (for example, proliferation, differentiation-induction or growth stimulation of megakaryocyte, platelet production, or phosphorylation of TPO receptor protein) is performed in the following manner. A test sample of the above-mentioned modified antibody is added to the cells which are expressing the antibody or cells into which the gene for the antibody has been introduced, and is evaluated by the change caused by the signal transduction (for example, human MPL antigen-specific proliferation, measurement of protein phosphorylation, or expression of platelet-specific antigen) using conventional methods.

**[0074]** In vivo evaluation is carried out by administering a monoclonal antibody recognizing MPL, a modified antibody of the invention and PBS as control to mice, and evaluating the strength of the activity by the change of the amount of platelet in mouse serum.

**[0075]** As mentioned above the modified antibodies of the invention can be obtained by preparing modified antibodies which contain two or more H chain V regions and two or more L chain V regions and specifically bind to TPO receptor and screening the modified antibodies by *in vivo* or *in vitro* evaluation as mentioned in the above.

**[0076]** The modified antibodies of the invention, which comprises two or more H chain V regions and two or more L chain V regions, preferably each two to four, more preferably each two, may be a dimer of the single chain Fv comprising one H chain V region and one L chain V region, or a single chain polypeptide in which two or more H chain V regions and two or more L chain V regions are connected. It is considered that owing to such construction the peptide mimics



three dimensional structure of TPO and therefore retains an excellent antigen-binding property and TPO agonist activity.

**[0077]** The modified antibodies of the invention have a remarkably lowered molecular size compared with parent antibody molecule (e.g. IgG), and, therefore, have a superior permeability into tissues and tumors and a higher activity than parent monoclonal antibody molecule. Therefore, the modified antibodies of the invention can efficiently transduce TPO signal into cells. The pharmaceutical preparations containing them are useful for treating platelet-reduction-related blood diseases and thrombocytopenia caused by chemotherapy for cancers or leukemia. It is further expected that the antibody of the invention can be used as a contrast agent by RI-labeling. The effect can be enhanced by attaching to a RI-compound or a toxin.

## BEST MODE FOR WORKING THE INVENTION

**[0078]** The present invention will concretely be illustrated in reference to the following examples, which in no way limit the scope of the invention.

**[0079]** For illustrating the production process of the modified antibodies of the invention, examples of producing single chain Fvs are shown below. Mouse antibodies against human IAP, MABL-1 and MABL-2 were used in the examples of producing the modified antibodies. Hybridomas MABL-1 and MABL-2 producing them respectively were internationally deposited as FERM BP-6100 and FERM BP-6101 with the National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology, Minister of International Trade and Industry (1-3 Higasi 1-chome, Tsukubashi, Ibaraki-ken, Japan), an authorized depository for microorganisms, on September 11, 1997.

### Examples

Comparative Example 1 (Cloning of DNAs encoding V region of mouse monoclonal antibodies to human IAP)

**[0080]** DNAs encoding variable regions of the mouse monoclonal antibodies to human IAP, MABL-1 and MABL-2, were cloned as follows.

#### 1.1 Preparation of messenger RNA (mRNA)

**[0081]** mRNAs of the hybridomas MABL-1 and MABL-2 were obtained by using mRNA Purification Kit (Pharmacia Biotech).

#### 1.2 Synthesis of double-stranded cDNA

**[0082]** Double-stranded cDNA was synthesized from about 1  $\mu$ g of the mRNA using Marathon cDNA Amplification Kit (CLONTECH) and an adapter was linked thereto.

#### 1.3 PCR Amplification of genes encoding variable regions of an antibody by

**[0083]** PCR was carried out using Thermal Cycler (PERKIN ELMER).

##### (1) Amplification of a gene coding for L chain V region of MABL-1

**[0084]** Primers used for the PCR method are Adapter Primer-1 (CLONTECH) shown in SEQ ID No. 1, which hybridizes to a partial sequence of the adapter, and MKC (Mouse Kappa Constant) primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 2, which hybridizes to the mouse kappa type L chain V region.

**[0085]** 50  $\mu$ l of the PCR solution contains 5  $\mu$ l of 10  $\times$  PCR Buffer II, 2 mM  $MgCl_2$ , 0.16 mM dNTPs (dATP, dGTP, dCTP and dTTP), 2.5 units of a DNA polymerase, AmpliTaq Gold (PERKIN ELMER), 0.2  $\mu$ M of the adapter primer of SEQ ID No. 1, 0.2  $\mu$ M of the MKC primer of SEQ ID No. 2 and 0.1  $\mu$ g of the double-stranded cDNA derived from MABL-1. The solution was preheated at 94°C of the initial temperature for 9 minutes and then heated at 94°C for 1 minute, at 60°C for 1 minute and at 72°C for 1 minute 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 10 minutes.

##### (2) Amplification of cDNA encoding H chain V region of MABL-1

**[0086]** The Adapter Primer-1 shown in SEQ ID No. 1 and MHC- $\gamma$ 1 (Mouse Heavy Constant) primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 3 were used as primers for PCR.

**[0087]** The amplification of cDNA was performed according to the method of the amplification of the L chain V region

gene, which was described in Example 1.3-(1), except for using 0.2  $\mu$ M of the MHC- $\gamma$ 1 primer instead of 0.2  $\mu$ M of the MKC primer.

### (3) Amplification of cDNA encoding L chain V region of MABL-2

**[0088]** The Adapter Primer-1 of SEQ ID No. 1 and the MKC primer of SEQ ID No. 2 were used as primers for PCR.

**[0089]** The amplification of cDNA was carried out according to the method of the amplification of the L chain V region gene of MABL-1 which was described in Example 1.3-(1), except for using 0.1  $\mu$ g of the double-stranded cDNA derived from MABL-2 instead of 0.1  $\mu$ g of the double-stranded cDNA from MABL-1.

### (4) Amplification of cDNA encoding H chain V region of MABL-2

**[0090]** The Adapter Primer-1 of SEQ ID No. 1 and MHC- $\gamma$ 2a. primer (Bio/Technology, 9, 88-89, 1991) shown in SEQ ID No. 4 were used as primers for PCR.

**[0091]** The amplification of cDNA was performed according to the method of the amplification of the L chain V region gene, which was described in Example 1.3-(3), except for using 0.2  $\mu$ M of the MHC- $\gamma$ 2a primer instead of 0.2  $\mu$ M of the MKC primer.

### 1.4 Purification of PCR products

**[0092]** The DNA fragment amplified by PCR as described above was purified using the QIAquick PCR Purification Kit (QIAGEN) and dissolved in 10 mM Tris-HCl (pH 8.0) containing 1 mM EDTA.

### 1.5 Ligation and Transformation

**[0093]** About 140 ng of the DNA fragment comprising the gene encoding the mouse kappa type L chain V region derived from MABL-1 as prepared above was ligated with 50 ng of pGEM-T Easy vector (Promega) in the reaction buffer comprising 30 mM Tris-HCl (pH 7.8), 10 mM  $MgCl_2$ , 10 mM dithiothreitol, 1 mM ATP and 3 units of T4 DNA Ligase (Promega) at 15°C for 3 hours.

**[0094]** Then, 1  $\mu$ l of the reaction mixture was added to 50  $\mu$ l of *E. coli* DH5 $\alpha$  competent cells (Toyobo Inc.) and the cells were stored on ice for 30 minutes, incubated at 42°C for 1 minute and stored on ice for 2 minutes again. 100  $\mu$ l of SOC medium (GIBCO BRL) was added. The cells of *E. coli* were plated on LB (Molecular Cloning: A Laboratory Manual, Sambrook et al., Cold Spring Harbor Laboratory Press, 1989) agar medium containing 100  $\mu$ g/ml of ampicillin (SIGMA) and cultured at 37°C overnight to obtain the transformant of *E. coli*.

**[0095]** The transformant was cultured in 3 ml of LB medium containing 50  $\mu$ g/ml of ampicillin at 37°C overnight and the plasmid DNA was prepared from the culture using the QIAprep Spin Miniprep Kit (QIAGEN).

**[0096]** The resulting plasmid comprising the gene encoding the mouse kappa type L chain V region derived from the hybridoma MABL-1 was designated as pGEM-M1L.

**[0097]** According to the same manner as described above, a plasmid comprising the gene encoding the mouse H chain V region derived from the hybridoma MABL-1 was prepared from the purified DNA fragment and designated as pGEM-M1H.

**[0098]** A plasmid comprising the gene encoding the mouse kappa type L chain V region derived from the hybridoma MABL-2 was prepared from the purified DNA fragment and designated as pGEM-M2L.

**[0099]** A plasmid comprising the gene encoding the mouse H chain V region derived from the hybridoma MABL-2 was prepared from the purified DNA fragment and designated as pGEM-M2H.

### Comparative Example 2 (DNA Sequencing)

**[0100]** The nucleotide sequence of the cDNA encoding region in the aforementioned plasmids was determined using Auto DNA Sequencer (Applied Biosystem) and ABI PRISM Dye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystem) according to the manufacturer's protocol.

**[0101]** The nucleotide sequence of the gene encoding the L chain V region from the mouse antibody MABL-1, which is included in the plasmid pGEM-M1L, is shown in SEQ ID No. 5.

**[0102]** The nucleotide sequence of the gene encoding the H chain V region from the mouse antibody MABL-1, which is included in the plasmid pGEM-M1H, is shown in SEQ ID No. 6.

**[0103]** The nucleotide sequence of the gene encoding the L chain V region from the mouse antibody MABL-2, which is included in the plasmid pGEM-M2L, is shown in SEQ ID No. 7.

**[0104]** The nucleotide sequence of the gene encoding the H chain V region from the mouse antibody MABL-2, which

is included in the plasmid pGEM-M2H, is shown in SEQ ID No. 8.

#### Comparative Example 3 (Determination of CDR)

**[0105]** The V regions of L chain and H chain generally have a similarity in their structures and each four framework regions therein are linked by three hypervariable regions, i.e., complementarity determining regions (CDR). An amino acid sequence of the framework is relatively well conserved, while an amino acid sequence of CDR has extremely high variation (Kabat, E.A., et al., "Sequences of Proteins of Immunological Interest", US Dept. Health and Human Services, 1983).

**[0106]** On the basis of these facts, the amino acid sequences of the variable regions from the mouse monoclonal antibodies to human IAP were applied to the database of amino acid sequences of the antibodies made by Kabat et al. to investigate the homology. The CDR regions were determined based on the homology as shown in Table 1.

Table 1

Plasmid	SEQ ID No.	CDR(1)	CDR(2)	CDR(3)
pGEM-M1L	5	43-58	74-80	113-121
pGEM-M1H	6	50-54	69-85	118-125
pGEM-M2L	7	43-58	74-80	113-121
pGEM-M2H	8	50-54	69-85	118-125

#### Comparative Example 4 (Identification of Cloned cDNA Expression

(Preparation of Chimera MABL-1 antibody and Chimera MABL-2 antibody.)

##### 4.1 Preparation of vectors expressing chimera MABL-1 antibody

**[0107]** cDNA clones, pGEM-M1L and pGEM-M1H, encoding the V regions of the L chain and the H chain of the mouse antibody MABL-1, respectively, were modified by the PCR method and introduced into the HEF expression vector (WO92/19759) to prepare vectors expressing chimera MABL-1 antibody.

**[0108]** A forward primer MLS (SEQ ID No. 9) for the L chain V region and a forward primer MHS (SEQ ID No. 10) for the H chain V region were designed to hybridize to a DNA encoding the beginning of the leader sequence of each V region and to contain the Kozak consensus sequence (J. Mol. Biol., 196, 947-950, 1987) and HindIII restriction enzyme site. A reverse primer MLAS (SEQ ID No. 11) for the L chain V region and a reverse primer MHAS (SEQ ID No. 12) for the H chain V region were designed to hybridize to a DNA encoding the end of the J region and to contain the splice donor sequence and BamHI restriction enzyme site.

**[0109]** 100  $\mu$ l of a PCR solution comprising 10  $\mu$ l of 10  $\times$  PCR Buffer II, 2 mM MgCl<sub>2</sub>, 0.16 mM dNTPs (dATP, dGTP, dCTP and dTTP), 5 units of DNA polymerase AmpliTaq Gold, 0.4  $\mu$ M each of primers and 8 ng of the template DNA (pGEM-M1L or pGEM-M1H) was preheated at 94°C of the initial temperature for 9 minutes and then heated at 94°C for 1 minute, at 60°C for 1 minute and at 72°C for 1 minute 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 10 minutes.

**[0110]** The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and then digested with HindIII and BamHI. The product from the L chain V region was cloned into the HEF expression vector, HEF- $\kappa$  and the product from the H chain V region was cloned into the HEF expression vector, HEF- $\gamma$ . After DNA sequencing, plasmids containing a DNA fragment with a correct DNA sequence are designated as HEF-M1L and HEF-M1H, respectively.

##### 4.2 Preparation of vectors expressing chimera MABL-2 antibodies

**[0111]** Modification and cloning of cDNA were performed in the same manner described in Example 4.1 except for using pGEM-M2L and pGEM-M2H as template DNA instead of pGEM-M1L and pGEM-M1H. After DNA sequencing, plasmids containing DNA fragments with correct DNA sequences are designated as HEF-M2L and HEF-M2H, respectively.

##### 4.3 Transfection to COS7 cells

**[0112]** The aforementioned expression vectors were tested in COS7 cells to observe the transient expression of the chimera MABL-1 and MABL-2 antibodies.

(1) Transfection with genes for the chimera MABL-1 antibody

**[0113]** COS7 cells were co-transformed with the HEF-M1L and HEF-M1H vectors by electroporation using the Gene Pulser apparatus (BioRad). Each DNA (10 µg) and 0.8 ml of PBS with  $1 \times 10^7$  cells/ml were added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25 µF of electric capacity.

**[0114]** After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into DMEM culture medium (GIBCO BRL) containing 10% γ-globulin-free fetal bovine serum. After culturing for 72 hours, the supernatant was collected, centrifuged to remove cell fragments and recovered.

(2) Transfection with genes coding for the chimera MABL-2 antibody

**[0115]** The co-transfection to COS7 cells with the genes coding for the chimera MABL-2 antibody was carried out in the same manner as described in Example 4.3-(1) except for using the HEF-M2L and HEF-M2H vectors instead of the HEF-M1L and HEF-M1H vectors. The supernatant was recovered in the same manner.

4.4 Flow cytometry

**[0116]** Flow cytometry was performed using the aforementioned culture supernatant of COS7 cells to measure binding to the antigen. The culture supernatant of the COS7 cells expressing the chimera MABL-1 antibody or the COS7 cells expressing the chimera MABL-2 antibody, or human IgG antibody (SIGMA) as a control was added to  $4 \times 10^5$  cells of mouse leukemia cell line L1210 expressing human IAP and incubated on ice. After washing, the FITC-labeled anti-human IgG antibody (Cappel) was added thereto. After incubating and washing, the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON).

**[0117]** Since the chimera MABL-1 and MABL-2 antibodies were specifically bound to L1210 cells expressing human IAP, it is confirmed that these chimera antibodies have proper structures of the V regions of the mouse monoclonal antibodies MABL-1 and MABL-2, respectively (Figs. 1-3).

Comparative Example 5 (Preparation of reconstructed Single chain Fv (scFv) of the antibody MABL-1 and antibody MABL-2)

5.1 Preparation of reconstructed single chain Fv of antibody MABL-1

**[0118]** The reconstructed single chain Fv of antibody MABL-1 was prepared as follows. The H chain V region and the L chain V of antibody MABL-1, and a linker were respectively amplified by the PCR method and were connected to produce the reconstructed single chain Fv of antibody MABL-1. The production method is illustrated in Fig. 4. Six primers (A-F) were employed for the production of the single chain Fv of antibody MABL-1. Primers A, C and E have a sense sequence and primers B, D and F have an antisense sequence.

**[0119]** The forward primer VHS for the H chain V region (Primer A, SEQ ID No. 13) was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain NcoI restriction enzyme recognition site. The reverse primer VHAS for H chain V region (Primer B, SEQ ID No. 14) was designed to hybridize to a DNA coding the C-terminal of the H chain V region and to overlap with the linker.

**[0120]** The forward primer LS for the linker (Primer C, SEQ ID No. 15) was designed to hybridize to a DNA encoding the N-terminal of the linker and to overlap with a DNA encoding the C-terminal of the H chain V region. The reverse primer LAS for the linker (Primer D, SEQ ID No. 16) was designed to hybridize to a DNA encoding the C-terminal of the linker and to overlap with a DNA encoding the N-terminal of the L chain V region.

**[0121]** The forward primer VLS for the L chain V region (Primer E, SEQ ID No. 17) was designed to hybridize to a DNA encoding the C-terminal of the linker and to overlap with a DNA encoding the N-terminal of the L chain V region. The reverse primer VLAS-FLAG for L chain V region (Primer F, SEQ ID No. 18) was designed to hybridize to a DNA encoding the C-terminal of the L chain V region and to have a sequence encoding the FLAG peptide (Hopp. T. P. et al., Bio/Technology, 6, 1204-1210, 1988), two stop codons and EcoRI restriction enzyme recognition site.

**[0122]** In the first PCR step, three reactions, A-B, C-D and E-F, were carried out and PCR products thereof were purified. Three PCR products obtained from the first PCR step were assembled by their complementarity. Then, the primers A and F were added and the full length DNA encoding the reconstructed single chain Fv of antibody MABL-1 was amplified (Second PCR). In the first PCR, the plasmid pGEM-M1H encoding the H chain V region of antibody MABL-1 (see Example 2), a plasmid pSC-DP1 which comprises a DNA sequence encoding a linker region comprising: Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser (SEQ ID No. 19) (Huston, J.S., et al., Proc. Natl. Acad. Sci. USA, 85, 5879-5883, 1988) and the plasmid pGEM-M1L encoding the L chain V region of antibody MABL-1 (see Example 2) were employed as template, respectively.

**[0123]** 50  $\mu$ l of the solution for the first PCR step comprises 5  $\mu$ l of 10  $\times$  PCR Buffer II, 2 mM MgCl<sub>2</sub>, 0.16 mM dNTPs, 2.5 units of DNA polymerase, AmpliTaq Gold (PERKIN ELMER), 0.4  $\mu$ M each of primers and 5 ng each of template DNA. The PCR solution was preheated at 94°C of the initial temperature for 9 minutes and then heated at 94°C for 1 minute, at 65°C for 1 minute and at 72°C for 1 minute and 20 seconds in order. This temperature cycle was repeated

35 times and then the reaction mixture was further heated at 72°C for 7 minutes.  
**[0124]** The PCR products A-B (371bp), C-D (63bp) and E-F (384bp) were purified using the QIAquick PCR Purification Kit (QIAGEN) and were assembled in the second PCR. In the second PCR, 98  $\mu$ l of a PCR solution comprising 120 ng of the first PCR product A-B, 20 ng of the PCR product C-D and 120 ng of the PCR product E-F, 10  $\mu$ l of 10  $\times$  PCR Buffer II, 2mM MgCl<sub>2</sub>, 0.16 mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (PERKIN ELMER) was preheated

at 94°C of the initial temperature for 8 minutes and then heated at 94°C for 2 minutes, at 65°C for 2 minutes and at 72°C for 2 minutes in order. This temperature cycle was repeated twice and then 0.4  $\mu$ M each of primers A and F were added into the reaction, respectively. The mixture was preheated at 94°C of the initial temperature for 1 minutes and then heated at 94°C for 1 minute, at 65°C for 1 minute and at 72°C for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 7 minutes.

**[0125]** A DNA fragment of 843 bp produced by the second PCR was purified and digested by NcoI and EcoRI. The resultant DNA fragment was cloned into pSCFVT7 vector. The expression vector pSCFVT7 contains a pelB signal sequence suitable for *E. coli* periplasmic expression-system (Lei, S.P., et al., J. Bacteriology, 169, 4379-4383, 1987). After the DNA sequencing, the plasmid containing the DNA fragment encoding correct amino acid sequence of the reconstructed single chain Fv of antibody MABL-1 is designated as "pscM1" (see Fig. 5). The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-1 contained in the plasmid pscM1 are shown in SEQ ID No. 20.

**[0126]** The pscM1 vector was modified by the PCR method to prepare a vector expressing the reconstructed single chain Fv of antibody MABL-1 in mammalian cells. The resultant DNA fragment was introduced into pCH01 expression vector. This expression vector, pCH01, was constructed by digesting DHFR- $\Delta$ E-rvH-PM1-f (WO92/19759) with EcoRI and SmaI to eliminate the antibody gene and connecting the EcoRI-NotI-BamHI Adapter (Takara Shuzo) thereto.

**[0127]** As a forward primer for PCR, Sal-VHS primer shown in SEQ ID No. 21 was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain Sall restriction enzyme recognition site. As a reverse primer for PCR, FRHlanti primer shown in SEQ ID No. 22 was designed to hybridize to a DNA encoding the end of the first framework sequence.

**[0128]** 100  $\mu$ l of PCR solution comprising 10  $\mu$ l of 10  $\times$  PCR Buffer II, 2 mM MgCl<sub>2</sub>, 0.16 mM dNTPs, 5 units of the DNA polymerase, AmpliTaq Gold, 0.4  $\mu$ l M each of primer and 8 ng of the template DNA (pscM1) was preheated at 95°C of the initial temperature for 9 minutes and then heated at 95°C for 1 minute, at 60°C for 1 minute and at 72°C for 1 minute and 20 seconds in order. This temperature cycle was repeated 35 times and then the reaction mixture was further heated at 72°C for 7 minutes.

**[0129]** The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by Sall and MboII to obtain a DNA fragment encoding the N-terminal of the reconstructed single chain Fv of antibody MABL-1. The pscM1 vector was digested by MboII and EcoRI to obtain a DNA fragment encoding the C-terminal of the reconstructed single chain Fv of antibody MABL-1. The Sall-MboII DNA fragment and the MboII-EcoRI DNA fragment were cloned into pCH01-Igs vector. After DNA sequencing, the plasmid comprising the desired DNA sequence was designated as "pCHOM1" (see Fig. 6). The expression vector, pCH01-Igs, contains a mouse IgG1 signal sequence suitable for the secretion-expression system in mammalian cells (Nature, 322, 323-327, 1988). The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-1 contained in the plasmid pCHOM1 are shown in SEQ ID No. 23.

## 5.2 Preparation of reconstructed single chain Fv of antibody MABL-2

**[0130]** The reconstructed single chain Fv of antibody MABL-2 was prepared in accordance with the aforementioned Example 5.1. Employed in the first PCR step were plasmid pGEM-M2H encoding the H chain V region of MABL-2 (see Example 2) instead of pGEM-M1H and plasmid pGEM-M2L encoding the L chain V region of MABL-2 (see Example 2) instead of pGEM-M1L, to obtain a plasmid pscM2 which comprises a DNA fragment encoding the desired amino acid sequence of the single chain Fv of antibody MABL-2. The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-2 contained in the plasmid pscM2 are shown in SEQ ID No. 24.

**[0131]** The pscM2 vector was modified by the PCR method to prepare a vector, pCHOM2, for the expression in mammalian cells which contains the DNA fragment encoding the correct amino acid sequence of reconstructed the single chain Fv of antibody MABL-2. The nucleotide sequence and the amino acid sequence of the reconstructed single chain Fv of antibody MABL-2 contained in the plasmid pCHOM2 are shown in SEQ ID No. 25.

### 5.3 Transfection to COS7 cells

**[0132]** The pCHOM2 vector was tested in COS7 cells to observe the transient expression of the reconstructed single chain Fv of antibody MABL-2.

**[0133]** The COS7 cells were transformed with the pCHOM2 vector by electroporation using the Gene Pulser apparatus (BioRad). The DNA (10 µg) and 0.8 ml of PBS with  $1 \times 10^7$  cells/ml were added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25 µF of electric capacity.

**[0134]** After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into IMDM culture medium (GIBCO BRL) containing 10% fetal bovine serum. After culturing for 72 hours, the supernatant was collected, centrifuged to remove cell fragments and recovered.

### 5.4 Detection of the reconstructed single chain Fv of antibody MABL-2 in culture supernatant of COS7 cells

**[0135]** The existence of the single chain Fv of antibody MABL-2 in the culture supernatant of COS7 cells which had been transfected with the pCHOM2 vector was confirmed by the Western Blotting method.

**[0136]** The culture supernatant of COS7 cells transfected with the pCHOM2 vector and the culture supernatant of COS7 cells transfected with the pCHO1 as a control were subjected to SDS electrophoresis and transferred to REINFORCED NC membrane (Schleicher & Schuell). The membrane was blocked with 5% skim milk (Morinaga Nyu-gyo), washed with 0.05% Tween 20-PBS and mixed with an anti-FLAG antibody (SIGMA). The membrane was incubated at room temperature, washed and mixed with alkaline phosphatase-conjugated mouse IgG antibody (Zymed). After incubating and washing at room temperature, the substrate solution (Kirkegaard Perry Laboratories) was added to develop color (Fig. 7).

**[0137]** A FLAG-peptide-specific protein was detected only in the culture supernatant of the pCHOM2 vector-introduced COS7 cells and thus it is confirmed that the reconstructed single chain Fv of antibody MABL-2 was secreted in this culture supernatant.

### 5.5 Flow cytometry

**[0138]** Flow cytometry was performed using the aforementioned COS7 cells culture supernatant to measure the binding to the antigen. The culture supernatant of the COS7 cells expressing the reconstructed single chain Fv of antibody MABL-2 or the culture supernatant of COS7 cells transformed with pCHO1 vector as a control was added to  $2 \times 10^5$  cells of the mouse leukemia cell line L1210 expressing human Integrin Associated Protein (IAP) or the cell line L1210 transformed with pCOS1 as a control. After incubating on ice and washing, the mouse anti-FLAG antibody (SIGMA) was added. Then the cells were incubated and washed. Then, the FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. Subsequently, the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

**[0139]** Since the single chain Fv of antibody MABL-2 was specifically bound to L1210 cells expressing human IAP, it is confirmed that the reconstructed single chain Fv of antibody MABL-2 has an affinity to human Integrin Associated Protein (IAP) (see Figs. 8-11).

### 5.6 Competitive ELISA

**[0140]** The binding activity of the reconstructed single chain Fv of antibody MABL-2 was measured based on the inhibiting activity against the binding of mouse monoclonal antibodies to the antigen.

**[0141]** The anti-FLAG antibody adjusted to 1 µg/ml was added to each well on 96-well plate and incubated at 37°C for 2 hours. After washing, blocking was performed with 1% BSA-PBS. After incubating and washing at a room temperature, the culture supernatant of COS7 cells into which the secretion-type human IAP antigen gene (SEQ ID No. 26) had been introduced was diluted with PBS into twofold volume and added to each well. After incubating and washing at a room temperature, a mixture of 50 µl of the biotinized MABL-2 antibody adjusted to 100 ng/ml and 50 µl of sequentially diluted supernatant of the COS7 cells expressing the reconstructed single chain Fv of antibody MABL-2 were added into each well. After incubating and washing at a room temperature, the alkaline phosphatase-conjugated streptavidin (Zymed) was added into each well. After incubating and washing at a room temperature, the substrate solution (SIGMA) was added and absorbance of the reaction mixture in each well was measured at 405 nm.

**[0142]** The results revealed that the reconstructed single chain Fv of antibody MABL-2 (MABL2-scFv.) evidently inhibited concentration-dependently the binding of the mouse antibody MABL-2 to human IAP antigen in comparison with the culture supernatant of the PCHO1-introduced COS7 cells as a control (Fig. 12). Accordingly, it is suggested that the reconstructed single chain Fv of antibody MABL-2 has the correct structure of each of the V regions from the mouse monoclonal antibody MABL-2.

### 5.7 Apoptosis-inducing Effect in vitro

**[0143]** An apoptosis-inducing action of the reconstructed single chain Fv of antibody MABL-2 was examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells transfected with human IAP gene, the L1210 cells transfected with the pCOS1 vector as a control and CCRF-CEM cells.

**[0144]** To each  $1 \times 10^5$  cells of the above cells was added the culture supernatant of the COS7 cells expressing the reconstructed single chain Fv of antibody MABL-2 or the culture supernatant of COS7 cells transfected with the pCHO1 vector as a control at 50% final concentration and the mixtures were cultured for 24 hours. Then, the Annexin-V staining was performed and the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

**[0145]** Results of the Annexin-V staining are shown in Figs. 13-18, respectively. Dots in the left-lower region represent living cells and dots in the right-lower region represent cells at the early stage of apoptosis and dots in the right-upper region represent cells at the late stage of apoptosis. The results show that the reconstructed single chain Fv of antibody MABL-2 (MABL2-scFv) remarkably induced cell death of L1210 cells specific to human IAP antigen (Figs. 13-16) and that the reconstructed single chain Fv also induced remarkable cell death of CCRF-CEM cells in comparison with the control (Figs. 17-18).

### 5.8 Expression of MABL-2 derived single chain Fv in CHO cells

**[0146]** CHO cells were transfected with the pCHOM2 vector to establish a CHO cell line which constantly expresses the single chain Fv (polypeptide) derived from the antibody MABL-2.

**[0147]** CHO cells were transformed with the pCHOM2 vector by the electroporation using the Gene Pulser apparatus (BioRad). A mixture of DNA (10  $\mu$ g) and 0.7 ml of PBS with CHO cells ( $1 \times 10^7$  cells/ml) was added to a cuvette. The mixture was treated with pulse at 1.5 kV, 25  $\mu$ F of electric capacity. After the restoration for 10 minutes at a room temperature, the electroporated cells were transferred into nucleic acid free  $\alpha$ -MEM medium (GIBCO BRL) containing 10% fetal bovine serum and cultured. The expression of desired protein in the resultant clones was confirmed by SDS-PAGE and a clone with a high expression level was selected as a cell line producing the single chain Fv derived from the antibody MABL-2. The cell line was cultured in serum-free medium CHO-S-SFM II (GIBCO BRL) containing 10 nM methotrexate (SIGMA). Then, the culture supernatant was collected, centrifuged to remove cell fragments and recovered.

### 5.9 Purification of MABL-2 derived single chain Fv produced in CHO cells

**[0148]** The culture supernatant of the CHO cell line expressing the single chain Fv obtained in Example 5.8 was concentrated up to twenty times using a cartridge for the artificial dialysis (PAN130SF, ASAHI MEDICALS). The concentrated solution was stored at -20°C and thawed on purification.

**[0149]** Purification of the single chain Fv from the culture supernatant of the CHO cells was performed using three kinds of chromatography, i.e., Blue-sepharose, a hydroxyapatite and a gel filtration.

#### (1) Blue-sepharose column chromatography

**[0150]** The concentrated supernatant was diluted to ten times with 20 mM acetate buffer (pH 6.0) and centrifuged to remove insoluble materials (10000  $\times$  rpm, 30 minutes). The supernatant was applied onto a Blue-sepharose column (20 ml) equilibrated with the same buffer. After washing the column with the same buffer, proteins adsorbed in the column were eluted by a stepwise gradient of NaCl in the same buffer, 0.1, 0.2, 0.3, 0.5 and up to 1.0 M. The pass-through fraction and each eluted fraction were analyzed by SDS-PAGE. The fractions in which the single chain Fv were confirmed (the fractions eluted at 0.1 to 0.3M NaCl) were pooled and concentrated up to approximately 20 times using CentriPrep-10 (AMICON).

#### (2) Hydroxyapatite

**[0151]** The concentrated solution obtained in (1) was diluted to 10 times with 10 mM phosphate buffer (pH 7.0) and applied onto the hydroxyapatite column (20 ml, BIORAD). The column was washed with 60 ml of 10 mM phosphate buffer (pH 7.0). Then, proteins adsorbed in the column were eluted by a linear gradient of sodium phosphate buffer up to 200 mM (see Fig. 19). The analysis of each fraction by SDS-PAGE confirmed the single chain Fv in fraction A and fraction B.

#### (3) Gel filtration

**[0152]** Each of fractions A and B in (2) was separately concentrated with CentriPrep-10 and applied onto TSKgel

G3000SWG column (21.5 × 600 mm) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl. Chromatograms are shown in Fig. 20. The analysis of the fractions by SDS-PAGE confirmed that both major peaks (AI and BI) are of desired single chain Fv. In the gel filtration analysis, the fraction A was eluted at 36 kDa of apparent molecular weight and the fraction B was eluted at 76 kDa. The purified single chain Fvs (AI, BI) were analyzed with 15% SDS polyacrylamide gel. Samples were treated in the absence or presence of a reductant and the electrophoresis was carried out in accordance with the Laemmli's method. Then the protein was stained with Coomassie Brilliant Blue. As shown in Fig. 21, both AI and BI gave a single band at 35 kDa of apparent molecular weight, regardless of the absence or presence of the reductant. From the above, it is concluded that AI is a monomer of the single chain Fv and BI is a non-covalently bound dimer of the single chain Fv. The gel filtration analysis of the fractions AI and BI with TSKgel G3000SW column (7.5 × 60 mm) revealed that a peak of the monomer is detected only in the fraction AI and a peak of the dimer is detected only in the fraction BI (Fig. 22). The dimer fraction (fraction BI) accounted for 4 percent (%) of total single chain Fvs. More than 90% of the dimer in the dimer fraction was stably preserved for more than a month at 4°C.

#### 5.10 Construction of vector expressing single chain Fv derived from antibody MABL-2 in *E. coli* cell

**[0153]** The pscM2 vector was modified by the PCR method to prepare a vector effectively expressing the single chain Fv from the antibody MABL-2 in *E. coli* cells. The resultant DNA fragment was introduced into pSCFVT7 expression vector.

**[0154]** As a forward primer for PCR, Nde-VHSm02 primer shown in SEQ ID No. 27 was designed to hybridize to a DNA encoding the N-terminal of the H chain V region and to contain a start codon and NdeI restriction enzyme recognition site. As a reverse primer for PCR, VLAS primer shown in SEQ ID No. 28 was designed to hybridize to a DNA encoding the C-terminal of the L chain V region and to contain two stop codons and EcoRI restriction enzyme recognition site. The forward primer, Nde-VHSm02, comprises five point mutations in the part hybridizing to the DNA encoding the N-terminal of the H chain V region for the effective expression in *E. coli*.

**[0155]** 100 µl of a PCR solution comprising 10 µl of 10 × PCR Buffer #1, 1 mM MgCl<sub>2</sub>, 0.2 mM dNTPs, 5 units of KOD DNA polymerase (all from TOYOBO), 1 µM of each primer and 100 ng of a template DNA (pscM2) was heated at 98°C for 15 seconds, at 65°C for 2 seconds and at 74°C for 30 seconds in order. This temperature cycle was repeated 25 times.

**[0156]** The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by NdeI and EcoRI, and then the resulting DNA fragment was cloned into pSCFVT7 vector, from which pelB signal sequence had been eliminated by the digestion with NdeI and EcoRI. After DNA sequencing, the resulting plasmid comprising a DNA fragment with the desired DNA sequence is designated as "pscM2DEm02" (see Fig. 23). The nucleotide sequence and the amino acid sequence of the single chain Fv derived from the antibody MABL-2 contained in the plasmid pscM2DEm02 are shown in SEQ ID No. 29.

#### 5.11 Expression of single chain Fv derived from antibody MABL-2 in *E. coli* cells

**[0157]** *E. coli* BL21 (DE3) pLysS (STRATAGENE) was transformed with pscM2DEm02 vector to obtain a strain of *E. coli* expressing the single chain Fv derived from antibody MABL-2. The resulting clones were examined for the expression of the desired protein using SDS-PAGE, and a clone with a high expression level was selected as a strain producing the single chain Fv derived from antibody MABL-2.

#### 5.12 Purification of single chain Fv derived from antibody MABL-2 produced in *E. coli*

**[0158]** A single colony of *E. coli* obtained by the transformation was cultured in 3 ml of LB medium at 28°C for 7 hours and then in 70 ml of LB medium at 28°C overnight. This pre-culture was transplanted to 7 L of LB medium and cultured at 28°C with stirring at 300 rpm using the Jarfermenter. When an absorbance of the medium reached O.D.=1.5, the bacteria were induced with 1 mM IPTG and then cultured for 3 hours.

**[0159]** The culture medium was centrifuged (10000 × g, 10 minutes) and the precipitated bacteria were recovered. To the bacteria was added 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl and 1% Triton X-100 and the bacteria were disrupted by ultrasonication (out put: 4, duty cycle: 70%, 1 minute × 10 times). The suspension of disrupted bacteria was centrifuged (12000 × g, 10 minutes) to precipitate inclusion body. Isolated inclusion body was mixed with 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl and 4% Triton X-100, treated by ultrasonication (out put: 4, duty cycle: 50%, 30 seconds × 2 times) again and centrifuged (12000 × g, 10 minutes) to isolate the desired protein as precipitate and to remove containment proteins included in the supernatant.

**[0160]** The inclusion body comprising the desired protein was lysed in 50 mM Tris-HCl buffer (pH 8.0) containing 6 M Urea, 5 mM EDTA and 0.1 M NaCl and applied onto Sephacryl S-300 gel filtration column (5 × 90 cm, Amersham Pharmacia) equilibrated with 50 mM Tris-HCl buffer (pH 8.0) containing 4M Urea, 5 mM EDTA, 0.1 M NaCl and 10 mM mercaptoethanol at a flow rate of 5 ml/minutes to remove associated single chain Fvs with high-molecular weight. The



obtained fractions were analyzed with SDS-PAGE and the fractions with high purity of the protein were diluted with the buffer used in the gel filtration up to  $O.D_{280}=0.25$ . Then, the fractions were dialyzed three times against 50 mM Tris-HCl buffer (pH 8.0) containing 5 mM EDTA, 0.1 M NaCl, 0.5 M Arg, 2 mM glutathione in the reduced form and 0.2 mM glutathione in the oxidized form in order for the protein to be refolded. Further, the fraction was dialyzed three times

against 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl to exchange the buffer.  
**[0161]** The dialysate product was applied onto Superdex 200 pg gel filtration column ( $2.6 \times 60$  cm, Amersham Pharmacia) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.15 M NaCl to remove a small amount of high molecular weight protein which was intermolecularly crosslinked by S-S bonds. As shown in Fig. 24, two peaks, major and sub peaks, were eluted after broad peaks which are expectedly attributed to an aggregate with a high molecular weight. The analysis by SDS-PAGE (see Fig. 21) and the elution positions of the two peaks in the gel filtration analysis suggest that the major peak is of the monomer of the single chain Fv and the sub peak is of the non-covalently bound dimer of the single chain Fv. The non-covalently bound dimer accounted for 4 percent of total single chain Fvs.

### 5.13 Apoptosis-inducing activity in vitro of single chain Fv derived from antibody MABL-2

**[0162]** An apoptosis-inducing action of the single chain' Fv from antibody MABL-2 (MABL2-scFv) produced by the CHO cells and *E. coli* was examined according to two protocols by Annexin-V staining (Boehringer Mannheim) using the L1210 cells (hIAP/L1210) into which human IAP gene had been introduced.

**[0163]** In the first protocol sample antibodies at the final concentration of 3  $\mu$ g/ml were added to  $5 \times 10^4$  cells of hIAP/L1210 cell line and cultured for 24 hours. Sample antibodies, i.e., the monomer and the dimer of the single chain Fv of MABL-2 from the CHO cells obtained in Example 5.9, the monomer and the dimer of the single chain Fv of MABL-2 from *E. coli* obtained in Example 5.12, and the mouse IgG antibody as a control were analyzed. After culturing, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON).

**[0164]** In the second protocol sample antibodies at the final concentration of 3  $\mu$ g/ml were added to  $5 \times 10^4$  cells of hIAP/L1210 cell line, cultured for 2 hours and mixed with anti-FLAG antibody (SIGMA) at the final concentration of 15  $\mu$ g/ml and further cultured for 22 hours. Sample antibodies of the monomer of the single chain Fv of MABL-2 from the CHO cells obtained in Example 5.9 and the mouse IgG antibody as a control were analyzed. After culturing, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus.

**[0165]** Results of the analysis by the Annexin-V staining are shown in Figs. 25-31. The results show that the dimers of the single chain Fv polypeptide of MABL-2 produced in the CHO cells and *E. coli* remarkably induced cell death (Figs. 26, 27) in comparison with the control (Fig. 25), while no apoptosis-inducing action was observed in the monomers of the single chain Fv polypeptide of MABL-2 produced in the CHO cells and *E. coli* (Figs. 28, 29). When anti-FLAG antibody was used together, the monomer of the single chain Fv polypeptide derived from antibody MABL-2 produced in the CHO cells induced remarkably cell death (Fig. 31) in comparison with the control (Fig. 30).

### 5.14 Antitumor effect of the monomer and the dimer of scFv/CHO polypeptide with a model mouse of human myeloma

#### (1) Quantitative measurement of human IgG in mouse serum

**[0166]** Measurement of human IgG (M protein) produced by human myeloma cell and contained in mouse serum was carried out by the following ELISA. 100  $\mu$ L of goat anti-human IgG antibody (BIOSOURCE, Lot#7902) diluted to 1  $\mu$ g/mL with 0.1% bicarbonate buffer (pH 9.6) was added to each well on 96 wells plate (Nunc) and incubated at 4°C overnight so that the antibody was immobilized. After blocking, 100  $\mu$ L of the stepwisely diluted mouse serum or human IgG (CAPPEL, Lot#00915) as a standard was added to each well and incubated for 2 hours at a room temperature. After washing, 100  $\mu$ L of alkaline phosphatase-labeled anti-human IgG antibody (BIOSOURCE, Lot#6202) which had been diluted to 5000 times was added, and incubation was carried out for 1 hour at a room temperature. After washing, a substrate solution was added. After incubation, absorbance at 405 nm was measured using the MICROPLATE READER Model 3550 (BioRad). The concentration of human IgG in the mouse serum was calculated based on the calibration curve obtained from the absorbance values of human IgG as the standard.

#### (2) Preparation of antibodies for administration

**[0167]** The monomer and the dimer of the scFv/CHO polypeptide were respectively diluted to 0.4 mg/mL or 0.25 mg/mL with sterile filtered PBS(-) on the day of administration to prepare samples for the administration.

(3) Preparation of a mouse model of human myeloma

**[0168]** A mouse model of human myeloma was prepared as follows. KPMM2 cells passaged in vivo (JP-Appl. 7-236475) by SCID mouse (Japan Clare) were suspended in RPMI1640 medium (GIBCO-BRL) containing 10% fetal bovine serum (GIBCO-BRL) and adjusted to  $3 \times 10^7$  cells/mL. 200  $\mu$ L of the KPMM2 cell suspension ( $6 \times 10^6$  cells/mouse) was transplanted to the SCID mouse (male, 6 week-old) via caudal vein thereof, which had been subcutaneously injected with the asialo GM1 antibody (WAKO JUNYAKU, 1 vial dissolved in 5 mL) a day before the transplantation.

(4) Administration of antibodies

**[0169]** The samples of the antibodies prepared in (2), the monomer (250  $\mu$ L) and the dimer (400  $\mu$ L), were administered to the model mice of human myeloma prepared in (3) via caudal vein thereof. The administration was started from three days after the transplantation of KPMM2 cells and was carried out twice a day for three days. As a control, 200  $\mu$ L of sterile filtered PBS(-) was likewise administered twice a day for three days via caudal vein. Each group consisted of seven mice.

(5) Evaluation of antitumor effect of the monomer and the dimer of scFv/CHO polypeptide with the model mouse of human myeloma

**[0170]** The antitumor effect of the monomer and the dimer of scFv/CHO polypeptide with the model mice of human myeloma was evaluated in terms of the change of human IgG (M protein) concentration in the mouse serum and survival time of the mice. The change of human IgG concentration was determined by measuring it in the mouse serum collected at 24 days after the transplantation of KPMM2 cells by ELISA described in the above (1). The amount of serum human IgG (M protein) in the serum of the PBS(-)-administered group (control) increased to about 8500  $\mu$ g/mL, whereas the amount of human IgG of the scFv/CHO dimer-administered group was remarkably low, that is, as low as one-tenth or less than that of the control group. Thus, the results show that the dimer of scFv/CHO strongly inhibits the growth of the KPMM2 cells (Fig. 32). As shown in Fig. 33, a remarkable elongation of the survival time was observed in the scFv/CHO dimer-administered group in comparison with the PBS(-)-administered group.

**[0171]** From the above, it is confirmed that the dimer of scFv/CHO has an antitumor effect for the human myeloma model mice. It is considered that the antitumor effect of the dimer of scFv/CHO, the modified antibody of the invention, results from the apoptosis-inducing action of the modified antibody.

5.15 Hemagglutination Test

**[0172]** Hemagglutination test and determination of hemagglutination were carried out in accordance with "Immuno-Biochemical Investigation", Zoku-Seikagaku Jikken Koza, edited by the Biochemical Society of Japan, published by Tokyo Kagaku Dojin.

**[0173]** Blood was taken from a healthy donor using heparin-treated syringes and washed with PBS(-) three times, and then erythrocyte suspension with a final concentration of 2% in PBS(-) was prepared. Test samples were the antibody MABL-2, the monomer and the dimer of the single chain Fv polypeptide produced by the CHO cells, and the monomer and the dimer of the single chain Fv polypeptide produced by *E. coli*, and the control was mouse IgG (ZYMED). For the investigation of the hemagglutination effect, round bottom 96-well plates available from Falcon were used. 50  $\mu$ L per well of the aforementioned antibody samples and 50  $\mu$ L of the 2% erythrocyte suspension were added and mixed in the well. After incubation for 2 hours at 37°C, the reaction mixtures were stored at 4°C overnight and the hemagglutination thereof was determined. As a control, 50  $\mu$ L per well of PBS(-) was used and the hemagglutination test was carried out in the same manner. The mouse IgG and antibody MABL-2 were employed at 0.01, 0.1, 1.0, 10.0 or 100.0  $\mu$ g/mL of the final concentration of the antibodies. The single chain Fvs were employed at 0.004, 0.04, 0.4, 4.0, 40.0 or 80.0  $\mu$ g/mL of the final concentration and further at 160.0  $\mu$ g/mL only in the case of the dimer of the polypeptide produced by *E. coli*. Results are shown in the Table 2. In the case of antibody MABL-2, the hemagglutination was observed at a concentration of more than 0.1  $\mu$ g/mL, whereas no hemagglutination was observed for both the monomer and the dimer of the single chain Fv.

Table 2 **Hemagglutination Test**

	Control	0.01	0.1	1	10	100	$\mu$ g/mL
mIgG	-	-	-	-	-	-	
MABL-2 (intact)	-	-	+	+++	+++	++	

(continued)

	Control	0.004	0.04	0.4	4	40	80	$\mu\text{g/mL}$
scFv/CHO monomer	-	-	-	-	-	-	-	
scFv/CHO dimer	-	-	-	-	-	-	-	
	Control	0.004	0.04	0.4	4	40	80	160 $\mu\text{g/mL}$
scFv/E.coli monomer	-	-	-	-	-	-	-	
scFv/E.coli dimer	-	-	-	-	-	-	-	

Comparative Example 6 Modified antibody  $\text{sc(Fv)}_2$  comprising two H chain V regions and two L chain V regions and antibody MABL-2 scFvs having linkers with different length

#### 6.1 Construction of plasmid expressing antibody MABL-2 $\text{sc(Fv)}_2$

**[0174]** For the preparation of a plasmid expressing the modified antibody  $[\text{sc(Fv)}_2]$  which comprises two H chain V regions and two L chain V regions derived from the antibody MABL-2, the aforementioned pCHOM2, which comprises the DNA encoding scFv derived from the MABL-2 described above, was modified by the PCR method as mentioned below and the resulting DNA fragment was introduced into pCHOM2.

**[0175]** Primers employed for the PCR are EF1 primer (SEQ ID NO: 30) as a sense primer, which is designed to hybridize to a DNA encoding EF1 $\alpha$ , and an antisense primer (SEQ ID NO: 19), which is designed to hybridize to the DNA encoding C-terminal of the L chain V region and to contain a DNA sequence coding for a linker region, and VLLAS primer containing Sall restriction enzyme recognition site (SEQ ID NO 31).

**[0176]** 100  $\mu\text{l}$  of the PCR solution comprises 10  $\mu\text{l}$  of  $10 \times$  PCR Buffer #1, 1 mM  $\text{MgCl}_2$ , 0.2 mM dNTPs (dATP, dGTP, dCTP and dTTP), 5 units of KOD DNA polymerase (Toyobo, Inc.), 1  $\mu\text{M}$  of each primer and 100 ng of the template DNA (pCHOM2). The PCR solution was heated at 94°C for 30 seconds, at 50°C for 30 seconds and at 74°C for 1 minute in order. This temperature cycle was repeated 30 times.

**[0177]** The PCR product was purified using the QIAquick PCR Purification Kit (QIAGEN) and digested by Sall. The resultant DNA fragment was cloned into pBluescript KS+ vector (Toyobo, Inc.). After DNA sequencing, a plasmid comprising the desired DNA sequence was digested by Sall and the obtained DNA fragment was connected using Rapid DNA Ligation Kit(BOEHRINGER MANNHEIM) to pCHOM2 digested by Sall. After DNA sequencing, a plasmid comprising the desired DNA sequence is designated as "pCHOM2(Fv) $_2$ " (see Fig. 34). The nucleotide sequence and the amino acid sequence of the antibody MABL-2  $\text{sc(Fv)}_2$  region contained in the plasmid pCHOM2(Fv) $_2$  are shown in SEQ ID No. 32.

#### 6.2 Preparation of Plasmid expressing antibody MABL-2 scFvs having linkers with-various length

**[0178]** The scFvs containing linkers with different length and the V regions which are designed in the order of [H chain]-[L chain] (hereinafter "HL") or [L chain]-[H chain] (hereinafter "LH") were prepared using, as a template, cDNAs encoding the H chain and the L chain derived from the MABL-2 as mentioned below.

**[0179]** To construct HL type scFv the PCR procedure was carried out using pCHOM2(Fv) $_2$  as a template. In the PCR step, a pair of CFHL-F1 primer (SEQ ID NO: 33) and CFHL-R2 primer (SEQ ID NO: 34) or a pair of CFHL-F2 primer (SEQ ID NO: 35) and CFHL-R1 primer (SEQ ID NO: 36) and KOD polymerase were employed. The PCR procedure was carried out by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order to produce a cDNA for the H chain containing a leader sequence at 5'-end or a cDNA for the L chain containing FLAG sequence at 3'-end thereof. The resultant cDNAs for the H chain and the L chain were mixed and PCR was carried out by repeating 5 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order using the mixture as templates and the KOD polymerase. To the reaction mixture were added CFHL-F1 and CFHL-R1 primers and then the PCR reaction was performed by repeating 30 times of the aforementioned temperature cycle to produce a cDNA for HL-0 type without a linker.

**[0180]** To construct LH type scFv, the PCR reaction was carried out using, as a template, pGEM-M2L and pGEM-M2H which contain cDNAs encoding the L chain V region and the H chain V region from the antibody MABL-2, respectively (see JP- Appl. 11-63557). A pair of T7 primer (SEQ ID NO: 37) and CFLH-R2 primer (SEQ ID NO: 38) or a pair of CFLH-F2 primer (SEQ ID NO: 39) and CFLH-R1 (SEQ ID NO: 40) and the KOD polymerase (Toyobo Inc.) were employed. The PCR reaction was performed by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in sequential order to produce a cDNA of an L chain containing a leader sequence at 5'-end or a cDNA of an H chain containing FLAG sequence at 3'-end thereof. The resultant cDNAs of the L chain and the H chain were mixed and PCR was carried out using this mixture as templates and the KOD polymerase by repeating

5 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order. To the reaction mixture were added T7 and CFLH-R1 primers and the reaction was performed by repeating 30 times of the aforementioned temperature cycle. The reaction product was used as a template and PCR was carried out using a pair of CFLH-F4 primer (SEQ ID NO: 41) and CFLH-R1 primer by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order to produce a cDNA of LH-0 type without a linker.

**[0181]** The resultant cDNAs of LH-0 and HL-0 types were digested by EcoRI and BamHI restriction enzymes (Takara Shuzo) and the digested cDNAs were introduced into an expression plasmid INPEP4 for mammalian cells using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* JM109 (Nippon Gene) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using QIAGEN Plasmid Maxi Kit (QIAGEN). Thus plasmids pCF2LH-0 and pCF2HL-0 were prepared.

**[0182]** To construct the expression plasmids of HL type containing linkers with different size, pCF2HL-0, as a template, and CFHL-X3 (SEQ ID NO: 42), CFHL-X4 (SEQ ID NO: 43), CFHL-X5 (SEQ ID NO: 44), CFHL-X6 (SEQ ID NO: 45) or CFHL-X7 (SEQ ID NO: 46), as a sense primer, and BGH-1 (SEQ ID NO: 47) primer, as an antisense primer, which is complementary with the vector sequence were employed. PCR reaction was carried out using the KOD polymerase by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order and the reaction products were digested by restriction enzymes XhoI and BamHI (Takara Shuzo). The digested fragments were introduced between XhoI and BamHI sites in the pCF2HL-0 using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* JM109 was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* by using Qiagen Plasmid Maxi kit. Thus expression plasmids pCF2HL-3, pCF2HL-4, pCF2HL-5, pCF2HL-6 and pCF2HL-7 were prepared.

**[0183]** To construct expression plasmid for the transient expression in COS7 cells the plasmids pCF2HL-0, pCF2HL-3, pCF2HL-4, pCF2HL-5, pCF2HL-6 and pCF2HL-7 were digested by restriction enzymes EcoRI and BamHI (Takara Shuzo) and the resultant fragments of approximately 800 bp were purified with agarose gel electrophoresis. The obtained fragments were introduced between EcoRI and BamHI sites in an expression plasmid pCOS1 for the expression in mammalian cells by using Ligation High (Toyobo Inc.), respectively. Competent *E. coli* DH5α (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using Qiagen Plasmid Maxi kit. Thus the expression plasmids CF2HL-0/pCOS1, CF2HL-3/pCOS1, CF2HL-4/pCOS1, CF2HL-5/pCOS1, CF2HL-6/pCOS1 and CF2HL-7/pCOS1 were prepared.

**[0184]** As a typical example of these plasmids, the construction of the plasmid CF2HL-0/pCOS1 is illustrated in Fig. 35 and the nucleotide sequence and the amino acid sequence of MABL2-scFv <HL-0> contained in the plasmid are shown in SEQ ID No. 48. Nucleotide sequences and amino acid sequences of the linker regions in these plasmids are also shown in Fig. 36.

**[0185]** To construct the expression plasmids of LH type containing linkers with different size, pCF2LH-0, as a template, and CFLH-X3 (SEQ ID NO: 49), CFLH-X4 (SEQ ID NO: 50), CFLH-X5 (SEQ ID NO: 51), CFLH-X6 (SEQ ID NO: 52) or CFLH-X7 (SEQ ID NO: 53), as a sense primer, and BGH-1 primer, as an antisense primer, which is complementary with the vector sequence were employed. PCR reaction was carried out using the KOD polymerase by repeating 30 times the temperature cycle consisting of 94°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute in order and the reaction products were digested by restriction enzymes XhoI and BamHI. The digested fragments were introduced into the pCF2LH-0 between XhoI and BamHI sites using Ligation High, respectively. Competent *E. coli* DH5α (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using Qiagen Plasmid Maxi kit. Thus expression plasmids pCF2LH-3, pCF2LH-4, pCF2LH-5, pCF2LH-6 and pCF2LH-7 were prepared.

**[0186]** To construct expression plasmid for the transient expression in COS7 cells the plasmids pCF2LH-0, pCF2LH-3, pCF2LH-4, pCF2LH-5, pCF2LH-6 and pCF2LH-7 were digested by restriction enzymes EcoRI and BamHI (Takara Shuzo) and the resultant fragments of approximately 800 bp were purified with agarose gel electrophoresis. The obtained fragments were introduced between XhoI and BamHI sites in an expression plasmid pCOS1 for the expression in mammalian cells by using the Ligation High, respectively. Competent *E. coli* DH5α (Toyobo Inc.) was transformed with each plasmid and the desired plasmids were isolated from the transformed *E. coli* using the Qiagen Plasmid Maxi kit. Consequently, the expression plasmids CF2LH-0/pCOS1, CF2LH-3/pCOS1, CF2LH-4/pCOS1, CF2LH-5/pCOS1, CF2LH-6/pCOS1 and CF2LH-7/pCOS1 were prepared.

**[0187]** As a typical example of these plasmids, the construction of the plasmid CF2LH-0/pCOS1 is illustrated in Fig. 37 and the nucleotide sequence and the amino acid sequence of MABL2-scFv <LH-0> contained in the plasmid are shown in SEQ ID No. 54. Nucleotide sequences and amino acid sequences of the linker regions in these plasmids are also shown in Fig. 38.

### 6.3 Expression of scFvs and sc(Fv)<sub>2</sub> in COS7 cells

(1) Preparation of culture supernatant using serum-containing culture medium .

**[0188]** The HL type and LH type of scFvs and sc(Fv)<sub>2</sub> were transiently expressed in COS7 cells (JCRB9127, Japan Health Sciences Foundation). COS7 cells were subcultured in DMEM media (GIBCO BRL) containing 10% fetal bovine serum (HyClone) at 37°C in carbon dioxide atmosphere incubator. The COS7 cells were transfected with CF2HL-0, 3 ~ 7/pCOS1, or CF2LH-0, 3 ~ 7/pCOS1 prepared in Example 6.2 or pCHOM2(Fv)<sub>2</sub> vectors by electroporation using the Gene Pulser apparatus (BioRad). The DNA (10 µg) and 0.25 ml of  $2 \times 10^7$  cells/ml in DMEM culture medium containing 10% FBS and 5 mM BES (SIGMA) were added to a cuvette. After standing for 10 minutes the mixtures were treated with pulse at 0.17kV, 950µF of electric capacity. After the restoration for 10 minutes at room temperature, the electroporated cells were transferred into the DMEM culture medium (10%FBS) in 75 cm<sup>3</sup> flask. After culturing for 72 hours, the culture supernatant was collected and centrifuged to remove cell fragments. The culture supernatant was subjected to the filtration using 0.22 µm bottle top filter (FALCON) to obtain the culture supernatant (hereinafter "CM").

(2) Preparation of culture supernatant using serum-free culture medium

**[0189]** Cells transfected in the same manner as (1) were transferred to the DMEM medium (10% FBS) in 75 cm<sup>3</sup> flask and cultured overnight. After the culture, the supernatant was discarded and the cells were washed with PBS and then added to CHO-S-SFM II medium (GIBCO BRL). After culturing for 72 hours, the culture supernatant was collected, centrifuged to remove cell fragments and filtered using 0.22 µm bottle top filter (FALCON) to obtain CM.

### 6.4 Detection of scFvs and sc(Fv)<sub>2</sub> in CM of COS7

**[0190]** The various MABL2-scFVs and sc(Fv)<sub>2</sub> in CM of COS7 prepared in the aforementioned Example 6.3 (2) were detected by Western Blotting method.

**[0191]** Each CM of COS7 was subjected to SDS-PAGE electrophoresis and transferred to REINFORCED NC membrane (Schleicher & Schuell). The membrane was blocked with 5% skim milk (Morinaga Nyu-gyo) and washed with TBS. Then an anti-FLAG antibody (SIGMA) was added thereto. The membrane was incubated at room temperature and washed. A peroxidase labeled mouse IgG antibody (Jackson Immuno Research) was added. After incubating and washing at room temperature, the substrate solution (Kirkegaard Perry Laboratories) was added to develop color (Fig. 39).

### 6.5 Flow cytometry

**[0192]** Flow cytometry was performed using the culture supernatants of COS7 cells prepared in Example 6.3 (1) to measure the binding of the MABL2-scFVs and sc(Fv)<sub>2</sub> to human, Integrin Associated Protein (IAP) antigen. The culture supernatants to be tested or a culture supernatant of COS7 cells as a control was added to  $2 \times 10^5$  cells of the mouse leukemia cell line L1210 expressing human IAP. After incubating on ice and washing, 10 µg/mL of the mouse anti-FLAG antibody (SIGMA) was added and then the cells were incubated and washed. Then, the FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. The fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON). The results of the flow cytometry show that the MABL2-scFvs having linkers with different length and the sc(Fv)<sub>2</sub> in the culture supernatants of COS7 have high affinity to human IAP (see Figs. 40a and 40b).

### 6.6 Apoptosis-inducing Effect in vitro

**[0193]** An apoptosis-inducing action of the culture supernatants of COS7 prepared in Example 6.3 (1) was examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells transfected with human IAP gene (hIAP/L1210).

**[0194]** To  $5 \times 10^4$  cells of the hIAP/L1210 cells were added the culture supernatants of COS7 cells transfected with each vectors or a culture supernatant of COS7 cells as a control at 10% of the final concentration and the mixtures were cultured for 24 hours. Then, the Annexin-V/PI staining was performed and the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON). The results revealed that scFvs <HL3, 4, 6, 7, LH3, 4, 6, 7> and sc(Fv)<sub>2</sub> in CM of COS7 induced remarkable cell death of hIAP/L1210 cells. These results are shown in Fig. 41.

### 6.7 Construction of vectors for the expression of scfvs and sc(Fv)<sub>2</sub> in CHO cells

**[0195]** To isolate and purify MABL2-scFvs and sc(Fv)<sub>2</sub> from culture supernatant, the expression vectors for expressing in CHO cells were constructed as below.

**[0196]** The EcoRI-BamHI fragments of pCF2HL-0, 3 - 7, and pCF2LH-0, 3 - 7 prepared in Example 6.2 were introduced between EcoRI and BamHI sites in an expression vector pCHO1 for CHO cells using the Ligation High. Competent *E. coli* DH5 $\alpha$  was transformed with them. The plasmids were isolated from the transformed *E. coli* using QIAGEN Plasmid Midi kit (QIAGEN) to prepare expression plasmids pCHOM2HL-0, 3 - 7, and pCHOM2LH-0, 3 - 7.

#### 6.8 Production of CHO cells expressing MABL2-scFvs <HL-0, 3 ~ 7>, MABL2-scFvs <LH-0, 3 ~ 7> and sc(Fv)<sub>2</sub> and preparation of the culture supernatants thereof

**[0197]** CHO cells were transformed with each of the expression plasmids pCHOM2HL-0, 3 ~ 7, and pCHOM2LH-0, 3 ~ 7, constructed in Example 6.7 and pCHOM2(Fv)<sub>2</sub> vector to prepare the CHO cells constantly expressing each modified antibody. As a typical example thereof, the production of the CHO cells constantly expressing MABL2-scFv <HL-5> or sc(Fv)<sub>2</sub> is illustrated as follows.

**[0198]** The expression plasmids pCHOM2HL-5 and pCHOM2(Fv)<sub>2</sub> were linearized by digesting with a restriction enzyme PvuI and subjected to transfection to CHO cells by electroporation using Gene Pulser apparatus (BioRad). The DNA (10  $\mu$ g) and 0.75 ml of PBS with  $1 \times 10^7$  cells/ml were added to a cuvette and treated with pulse at 1.5 kV, 25  $\mu$ F of electric capacity. After the restoration for 10 minutes at room temperature, the electroporated cells were transferred into nucleic acid-containing  $\alpha$ -MEM culture medium (GIBCO BRL) containing 10% fetal bovine serum and cultured. After culturing overnight, the supernatant was discarded. The cells were washed with PBS and added to nucleic acid-free  $\alpha$ -MEM culture medium (GIBCO BRL) containing 10% fetal bovine serum. After culturing for two weeks, the cells were cultured in a medium containing 10 nM (final concentration) methotrexate (SIGMA), then 50 nM and 100 nM methotrexate. The resultant cells were cultured in serum-free CHO-S-SFM II medium (GIBCO BRL) in a roller bottle. The culture supernatant was collected, centrifuged to remove cell fragments and filtered using a filter with 0.22  $\mu$ m of pore size to obtain CM, respectively.

**[0199]** According to the above, CHO cells which constantly express MABL2-scFvs <HL-0, -3, -4, -6, -7> and <LH-0, -3, -4, -5, -6, -7> and CMs thereof were obtained.

#### 6.9 Purification of dimer of MABL2-scFv <HL-5> and sc(Fv)<sub>2</sub>

**[0200]** The MABL2-scFv <HL-5> and the sc(Fv)<sub>2</sub> were purified from CMs prepared in Example 6.8 by two types of purification method as below.

##### <Purification Method 1>

**[0201]** HL-5 and sc(Fv)<sub>2</sub> were purified by the anti-FLAG antibody affinity column chromatography utilizing the FLAG sequence located at C-terminal of the polypeptides and by gel filtration. One liter of CM as obtained in 6.8 was applied onto a column (7.9ml) prepared with anti-FLAG M2 Affinity gel (SIGMA) equilibrated with 50 mM Tris-HCl buffer (TBS, pH 7.5) containing 150 mM NaCl. After washing the column with TBS, the scFv was eluted by 0.1 M glycine-HCl buffer, pH 3.5. The resultant fractions were analyzed by SDS-PAGE and the elution of the scFv was confirmed. The scFv fraction was mixed with Tween 20 up to 0.01% of the final concentration and concentrated using Centricon-10 (MILLIPORE). The concentrate was applied onto TSKgel G3000SWG column (7.5  $\times$  600 mm) equilibrated with 20 mM acetate buffer (pH 6.0) containing 150 mM NaCl and 0.01% Tween 20. At 0.4 mL/minute of the flow rate, the scFv was detected by the absorption at 280 nm. The HL-5 was eluted as the major fraction in the position of the dimer and the sc(Fv)<sub>2</sub> was eluted in the position of the monomer.

##### <Purification Method 2>

**[0202]** HL-5 and sc(Fv)<sub>2</sub> were purified using three steps comprising ion exchange chromatography, hydroxyapatite and gel filtration. In the ion exchange chromatography, Q sepharose fast flow column (Pharmacia) was employed for HL-5 and SP-sepharose fast flow column was employed for sc(Fv)<sub>2</sub>. In and after the second step, HL-5 and sc(Fv)<sub>2</sub> were processed by the same procedure.

##### First step for HL-5

**[0203]** CM of HL-5 was diluted to two times with 20 mM Tris-HCl buffer (pH 9.0) containing 0.02% Tween 20 and then the pH was adjusted to 9.0 with 1 M Tris. The solution was applied onto Q Sepharose fast flow column equilibrated with 20 mM Tris-HCl buffer (pH 8.5) containing 0.02% Tween 20. A polypeptide adsorbed to the column was eluted by a linear gradient of NaCl in the same buffer, from 0.1 to 0.55 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing HL-5 were collected and subjected to hydroxyapatite of the second step.

First step for sc(Fv)<sub>2</sub>

**[0204]** CM of the sc(Fv)<sub>2</sub> was diluted to two times with 20mM acetate buffer (pH 5.5) containing 0.02% Tween 20 and its pH was adjusted to 5.5 with 1 M acetic acid. The solution was applied onto a SP-Sepharose fast flow column equilibrated with 20 mM acetate buffer (pH 5.5) containing 0.02% Tween 20. A polypeptide adsorbed to the column was eluted by a linear gradient of NaCl in the buffer, from 0 to 0.5 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing the sc(Fv)<sub>2</sub> were collected and subjected to hydroxyapatite of the second step.

Second step: Hydroxyapatite chromatography of HL-5 and sc(Fv)<sub>2</sub>

**[0205]** The fractions of HL-5 and sc(Fv)<sub>2</sub> obtained in the first step were separately applied onto the hydroxyapatite column (Type I, BIORAD) equilibrated with 10 mM phosphate buffer containing 0.02% Tween 20, pH 7.0. After washing the column with the same buffer, polypeptides adsorbed to the column were eluted by a linear gradient of the phosphate buffer up to 0.5 M. Monitoring the eluted fractions by SDS-PAGE, the fractions containing the desired polypeptides were collected.

Third step: Gel filtration of HL-5 and sc(Fv)<sub>2</sub>

**[0206]** Each fraction obtained at the second step was separately concentrated with CentriPrep-10 (MILIPORE) and applied onto a Superdex 200 column (2.6 × 60 cm, Pharmacia) equilibrated with 20 mM acetate buffer (pH 6.0) containing 0.02% Tween 20 and 0.15 M NaCl. HL-5 was eluted in the position of the dimer, and sc(Fv)HL-5. and sc(Fv)<sub>2</sub> were eluted in the position of the monomer as a major peak respectively.

**[0207]** Since the monomer of HL-5 was hardly detected by both purification methods, it is proved that the dimers of single chain Fvs are formed in high yields when the linker for the single chain Fv contains around 5 amino acids. Furthermore, the dimer of HL-5 and the sc(Fv)<sub>2</sub> were stably preserved for a month at 4°C after the purification.

6.10 Evaluation of the binding activity of purified dimer of scFv <HL-5> and sc(Fv)<sub>2</sub> against antigen

**[0208]** Flow cytometry was performed using the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)<sub>2</sub> in order to evaluate the binding to human Integrin Associated Protein (IAP), antigen. 10 μg/ml of the purified dimer of MABL2-scFv <HL-5>, the purified sc(Fv)<sub>2</sub>, the antibody MABL-2 as a positive control or a mouse IgG (Zymed) as a negative control was added to 2 × 10<sup>5</sup> cells of the mouse leukemia cell line L1210 expressing human IAP (hIAP/L1210) or the cell line L1210 transformed with pCOS1 (pCOS1/L1210) as a control. After incubating on ice and washing, 10 μg/mL of the mouse anti-FLAG antibody (SIGMA) was added and then the cells were incubated and washed. FITC labeled anti-mouse IgG antibody (BECTON DICKINSON) was added thereto and the cells were incubated and washed again. Then the fluorescence intensity was measured using the FACScan apparatus (BECTON DICKINSON).

**[0209]** Since the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)<sub>2</sub> were specifically bound to hIAP/L1210 cells, it is confirmed that the dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> have high affinity to human IAP (see Fig. 42).

6.11 Apoptosis-inducing activity in vitro of purified dimer of scFv <HL-5> and sc(Fv)<sub>2</sub>

**[0210]** An apoptosis-inducing action of the purified dimer of MABL2-scFv <HL-5> and the purified sc(Fv)<sub>2</sub> were examined by Annexin-V staining (Boehringer Mannheim) using the L1210 cells (hIAP/L1210) in which human IAP gene had been introduced and cells of human leukemic cell line CCRF-CEM.

**[0211]** Different concentrations of the purified dimer of MABL2-scFv <HL-5>, the purified MABL2-sc(Fv)<sub>2</sub>, the antibody MABL-2 as a positive control or a mouse IgG as a negative control were added to 5 × 10<sup>4</sup> cells of hIAP/L1210 cell line or 1 × 10<sup>5</sup> cells of CCRF-CEM cell line. After culturing for 24 hours, the Annexin-V staining was carried out and the fluorescence intensity thereof was measured using the FACScan apparatus (BECTON DICKINSON). As a result the dimer of MABL2-scFv <HL-5> and the MABL2-sc(Fv)<sub>2</sub> remarkably induced cell death of hIAP/L1210 and CCRF-CEM in concentration-dependent manner (see Fig. 43). As a result it was shown that the dimer of MABL2-scFv <HL-5> and MABL2-sc(Fv)<sub>2</sub>, had improved efficacy of inducing apoptosis compared with original antibody MABL-2.

6.12 Hemagglutination Test of the purified dimer of scFv <HL-5> and the sc (Fv)<sub>2</sub>

**[0212]** Hemagglutination test was carried out using different concentrations of the purified dimer of scFv <HL-5> and the purified sc(Fv)<sub>2</sub> in accordance with Example 5.15.

**[0213]** The hemagglutination was observed with the antibody MABL-2 as a positive control, whereas no hemagglutination was observed with both the single chain antibody MABL2-sc(Fv)<sub>2</sub> and the MABL2-scFv <HL-5>. Further, there

# EP 1 327 680 B1

was no substantial difference in the hemagglutination between two buffers employed with the antibody MABL-2. These results are shown in Table 3.

5

10

15

20

25

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35

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45

50

55



TABLE 3

**Hemagglutination Test**  
**Diluent : PBS**

	cont	28.9	14.45	7.225	3.6125	1.8063	0.9031	0.4516	0.2258	0.1129	0.0564	0.0282	0.0141	0.0071	0.0035	0.0018
<b>MABL2-sc(Fv)<sub>2</sub></b>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	(µg/ml)															
	cont	28.0	14.0	7.0	3.5	1.75	0.875	0.4375	0.2188	0.1094	0.0547	0.0273	0.0137	0.0068	0.0034	0.0017
<b>MABL2s c(Fv) &lt;HL5&gt;</b>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	(µg/ml)															
	cont	80	40	20	10	5	2.5	1.25	0.625	0.3125	0.1563	0.0781	0.0391	0.0195	0.0098	0.0049
<b>MABL2 (Intact) mlgG</b>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	(µg/ml)															
<b>Diluent: Acetate Buffer</b>																
	cont	80	40	20	10	5	2.5	1.25	0.625	0.3125	0.1563	0.0781	0.0391	0.0195	0.0098	0.0049
<b>MABL2 (Intact)</b>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

6.13 Antitumor effect of the purified dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> for a model mouse of human myeloma

[0214] The antitumor effects were tested for the dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> prepared and purified in Examples 6.8 and 6.9. The test was performed by using the mouse model for human myeloma produced in Example 5.1 and determining the amount of M protein produced by human myeloma cells in the mouse serum using ELISA and examining survival time of the mice. Then, the antitumor effects of the dimer of scFv <HL-5> and the sc(Fv)<sub>2</sub> were evaluated in terms of the change of the amount of M protein in the mouse serum and the survival time of the mice.

[0215] In the test, the HL-5 and the sc(Fv)<sub>2</sub> were employed as a solution at 0.01, 0.1 or 1-mg/mL in vehicle consisting of 150 mM NaCl, 0.02% Tween and 20 mM acetate buffer, pH 6.0 and administered to the mice at 0.1, 1 or 10 mg/kg of dosage. Control group of mice were administered only with the vehicle.

[0216] The mouse serum was gathered 26 days after the transplantation of the human myeloma cells and the amount of M protein in the serum was measured using ELISA according to Example 5.14. As a result, the amount of M protein in the serum of both mice groups administered with HL-5, the dimer and the sc(Fv)<sub>2</sub> decreased in dose-dependent manner (see Fig. 44). Furthermore, a significant elongation of the survival time was observed in both groups administered with the HL-5 (Fig. 45) and with the sc(Fv)<sub>2</sub> (Fig. 46) in comparison with the control group administered with the vehicle. These results show that the HL-5 and the sc(Fv)<sub>2</sub> of the invention have excellent antitumor effect in vivo.

## Example 7

Single chain Fv comprising H chain V region and L chain V region of human antibody 12B5 against human MPL

[0217] A DNA encoding V regions of human monoclonal antibody 12B5 against human MPL was constructed as follows:

## 7.1 Construction of a gene encoding H chain V-region of 12B5

[0218] The gene encoding H chain V region of human antibody 12B5 binding to human MPL was designed by connecting the nucleotide sequence of the gene thereof (SEQ ID NO: 55) at the 5'-end to the leader sequence (SEQ ID NO: 56) originated from human antibody gene (Eur. J. Immunol. 1996; 26: 63-69). The designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12B5VH-1, 12B5VH-2, 12B5VH-3, 12B5VH-4). 12B5VH-1 (SEQ ID NO: 57) and 12B5VH-3 (SEQ ID NO: 59) were synthesized in the sense direction, and 12B5VH-2 (SEQ ID NO: 58) and 12B5VH-4 (SEQ ID NO: 60) in the antisense direction, respectively. After assembling each synthesized oligonucleotide by respective complementarity, the outside primers (12B5VH-S and 12B5VH-A) were added to amplify the full length of the gene. 12B5VH-S (SEQ ID NO: 61) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have Hind III restriction enzyme recognition site and Kozak sequence, and 12B5VH-A (SEQ ID NO: 62) was designed to hybridize to the nucleotide sequence encoding C-terminal of H chain V region by the reverse primer and to have a splice donor sequence and BamHI restriction enzyme recognition site, respectively.

[0219] 100 µl of the PCR solution containing 10 µl of 10 × PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs (dATP, dGTP, dCTP, dTTP), 5 units of DNA-polymerase AmpliTaq Gold (all by PERKIN ELMER) and each 2.5 p mole of each synthesized oligonucleotide (12B5VH-1 to -4) was heated at 94°C of the initial temperature for 9 minutes, at 94°C for 2 minutes, at 55°C for 2 minutes and 72°C for 2 minutes. After repeating the cycle two times each 100 pmole of external primer 12B5VH-S and 12B5VH-A was added. The mixture was subjected to the cycle consisting of at 94°C for 30 seconds, at 55°C for 30 seconds and 72°C for 1 minute 35 times and heated at 72°C for further 5 minutes.

[0220] The PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes BamHI and Hind III, and cloned into expression vector HEF-gyl for human H chain. After determining the DNA sequence the plasmid containing the correct DNA sequence was named HEF-12B5H-gy1.

[0221] The HEF-12B5H-gy1 was digested by restriction enzymes EcoRI and BamHI to produce the gene encoding 12B5VH which was then cloned into an expression vector pCOS-Fd for human Fab H chain to produce pFd-12B5H. The expression vector for human Fab H chain was constructed by amplifying the DNA (SEQ ID NO: 63) containing the intron region existing between the genes encoding human antibody H chain V region and the constant region, and the gene encoding a part of the constant region of human H chain by PCR, and inserting the PCR product into animal cell expression vector pCOS1. The human H chain constant region was amplified for the gene under the same conditions mentioned above using as the template HEF-gy1, as the forward primer G1CH1-S (SEQ ID NO: 64) which was designed to hybridize to 5'-end sequence of intron 1 and to have restriction enzyme recognition sites EcoRI and BamHI and as the reverse primer G1CH1-A (SEQ ID NO: 65) which was designed to hybridize to 3'-end DNA of human H chain constant region CH1 domain and to have a sequence encoding a part of hinge region, two stop codons and restriction enzyme recognition site Bg1 II.

[0222] The nucleotide sequence and amino acid sequence of the reconstructed 12B5H chain variable region which

were included in plasmids HEF-12B5H-gyl and pFd-12B5H are shown in SEQ ID NO: 66.

## 7.2 Construction of the gene encoding 12B5 L chain V region

**[0223]** The gene encoding L chain V region of human antibody 12B5 binding to human MPL was designed by connecting the nucleotide sequence of gene (SEQ ID NO: 67) at the 5'-end to the leader sequence (SEQ ID NO: 68) originated from human antibody gene 3D6 (Nuc. Acid Res. 1990: 18; 4927). In the same way as mentioned above the designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12B5VL-1, 12B5VL-2, 12B5VL-3, 12B5VL-4) and synthesized respectively. 12B5VL-1 (SEQ ID NO: 69) and 12B5VL-3 (SEQ ID NO: 71) had sense sequences, and 12B5VL-2 (SEQ ID NO: 70) and 12B5VL-4 (SEQ ID NO: 72) had antisense sequences, respectively. Each of the synthesized oligonucleotides was assembled by respective complementarity and mixed with the external primer (12B5VL-S and 12B5VL-A) to amplify the full length of the gene. 12B5VL-S (SEQ ID NO: 73) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have Hind III restriction enzyme recognition site and Kozak sequence. 12B5VL-A (SEQ ID NO: 74) was designed to hybridize to the nucleotide sequence encoding C-terminal of L chain V region by the reverse primer and to have a splice donor sequence and BamHI restriction enzyme recognition site.

**[0224]** Performing the PCR as mentioned above, the PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes BamHI and Hind III, and cloned into an expression vector HEF-gk for human L chain. After determining the DNA sequence the plasmid containing the correct DNA sequence was named HEF-12B5L-gk. The nucleotide sequence and amino acid sequence of the reconstructed 12B5 L chain V region which were included in plasmid HEF-12B5L-gk are shown in SEQ ID NO:75.

## 7.3 Production of reconstructed 12B5 single chain Fv (scFv)

**[0225]** The reconstructed 12B5 antibody single chain Fv was designed to be in the order of 12B5VH-linker-12B5VL and to have FLAG sequence (SEQ ID NO: 76) at C-terminal to facilitate the detection and purification. The reconstructed 12B5 single chain Fv (sc12B5) was constructed using a linker sequence consisting of 15 amino acids represented by (Gly<sub>4</sub>Ser)<sub>3</sub>.

### (1) Production of the reconstructed 12B5 single chain Fv using the linker sequence consisting of 15 amino acids

**[0226]** The gene encoding the reconstructed 12B5 antibody single chain Fv, which contained the linker sequence consisting of 15 amino acids, was constructed by connecting 12B5 H chain V region, linker region and 12B5 L chain V region which was amplified by PCR respectively. This method is schematically shown in Fig. 47. Six PCR primers (A-F) were used for production of the reconstructed 12B5 single chain Fv. Primers A, C, and E had sense sequences, and primers B, D, and F had antisense sequences.

**[0227]** The forward primer 12B5-S (Primer A, SEQ ID NO: 77) for H chain V region was designed to hybridize to 5'-end of H chain leader sequence and to have EcoRI restriction enzyme recognition site. The reverse primer HuVHJ3 (Primer B, SEQ ID NO: 78) for H chain V region was designed to hybridize to DNA encoding C-terminal of H chain V region.

**[0228]** The forward primer RHuJH3 (Primer C, SEQ ID NO: 79) for the linker was designed to hybridize to DNA encoding the N-terminal of the linker and to overlap DNA encoding the C-terminal of H chain V region. The reverse primer RHuVK1 (Primer D, SEQ ID NO: 80) for the linker was designed to hybridize to DNA encoding the C-terminal of the linker and overlap DNA encoding the N-terminal of L chain V region.

**[0229]** The forward primer HuVK1.2 (Primer E, SEQ ID NO: 81) for L chain V region was designed to hybridize to DNA encoding the N-terminal of L chain V region. The reverse primer 12B5F-A for L chain V region (Primer F, SEQ ID NO: 82) was designed to hybridize to DNA encoding C-terminal of L chain V region and to have the sequence encoding FLAG peptide (Hopp, T. P. et al., Bio/Technology, 6, 1204-1210, 1988), two transcription stop codons and NotI restriction enzyme recognition site.

**[0230]** In the first PCR step, three reactions A-B, C-D, and E-F were performed, and the three PCR products obtained from the first step PCR were assembled by respective complementarity. After adding primers A and F the full length DNA encoding the reconstructed 12B5 single chain Fv having the linker consisting of 15 amino acids was amplified (the second PCR). In the first step PCR, the plasmid HEF-12B5H-gyl (see Example 7. 1) encoding the reconstructed 12B5 H chain V region, pSCFVT7-hM21 (humanized ONS-M21 antibody) (Ohtomo et al., Anticancer Res. 18 (1998), 4311-4316) containing DNA (SEQ ID NO: 83) encoding the linker region consisting of Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser (Huston et al., Proc. Natl. Acad. Sci. USA, 85, 5879-5883, 1988) and the plasmid HEF-12B5L-gk (see Example 7. 2) encoding the reconstructed 12B5 L chain V region were used as templates, respectively.

**[0231]** 50μl of PCR solution for the first step contained 5μl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (all by PERKIN ELMER), each 100 pmole of each primer and 100ng of each

template DNA. The PCR solution was heated at 94°C of the initial temperature for 9 minutes, at 94 for 30 seconds, 55°C for 30 seconds and 72°C for 1 minute. After repeating the cycle 35 times the reaction mixture was further heated 72°C for 5 minutes.

[0232] The PCR products A-B, C-D, and E-F were assembled by the second PCR. PCR mixture solution for the second step of 98µl containing as the template 1µl of the first PCR product A-B, 0.5µl of PCR product C-D and 1µl of PCR product E-F, 10µl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (all by PERKIN ELMER) was heated at 94°C of the initial temperature for 9 minutes, at 94°C for 2 minutes, at 65°C for 2 minutes and 72°C for 2 minutes. After repeating the cycle two times, each 100 pmole of each of primers A and F were added. After repeating the cycle consisting of at 94°C for 30 seconds, 55°C for 30 seconds and 72°C for 1 minute 35 times, the reaction mixture was heated at 72°C for 5 minutes.

[0233] The DNA fragments produced by the second PCR were purified using 1.5% low-melting-temperature agarose gel, digested by EcoRI and NotI, and cloned into pCHO1 vector and pCOS1 vector (Japanese Patent Application No. 8-255196). The expression vector pCHO1 was a vector constructed by deleting the antibody gene from DHFR-ΔE-rvH-PM1-f (see WO92/19759) by EcoRI and SmaI digestion, and connecting to EcbRI-NotI-BamHI Adaptor (TAKARA SHUZO). After determining the DNA sequence the plasmids containing the DNA fragment encoding the correct amino acid sequence of reconstructed 12B5 single chain Fv were named pCHO-sc12B5 and pCOS-sc12B5. The nucleotide sequence and amino acid sequence of the reconstructed 12B5 single chain Fv included in the plasmids pCHO-sc12B5 and pCOS-sc12B5 are shown in SEQ ID NO: 84.

#### 7-4 Expression of antibody 12B5 (IgG, Fab) and single chain Fv polypeptide by animal cell

[0234] Antibody 12B5 (IgG, Fab) and single chain Fv derived from antibody 12B5 were expressed by using COS-7 cells or CHO cells.

[0235] The transient expression using COS-7 cells was performed as follows. The transfection was performed by electroporation method using Gene Pulser equipment (BioRad). For the expression of antibody 12B5 (IgG) each 10µg of the above-mentioned expression vector HEF-12B5H-gy1 and HEF-12 B5L-gk were added, for the expression of 12B5Fab fragment each 10µg of pFd-12B5H and HEF-12B5L-gk were added and for the expression of single chain Fv 10µg of pCOS-sc12B5 was added to COS-7 cells ( $1 \times 10^7$  cells/ml) suspended in 0.8ml of PBS. The mixture kept in a cuvette was treated by pulse at the capacity of 1.5kV, 25µFD. After recovering for 10 minutes in a room temperature the electroporated cells were added to DMEM culture medium (GIBCO BRL) containing 10% bovine fetal serum cultivated. After cultivating overnight the cells were washed once by PBS, added to serum-free medium CHO-S-SFM II and cultivated for 2 days. The culture medium was centrifuged to remove cell debris and filtered with 0.22µm filter to prepare the culture supernatant.

[0236] To establish a stable expression CHO cell line for the single chain Fv (polypeptide) derived from antibody 12B5, the expression vector pCHO-sc12B5 was introduced into CHO cells as follows.

[0237] The expression vector was introduced into CHO cells by electroporation method using Gene Pulser equipment (BioRad). Linearized DNA (100µg) obtained by digestion with restriction enzyme PvuI and CHO cells ( $1 \times 10^7$  cells/ml) suspended in 0.8 ml of PBS were mixed in a cuvette, left stationary on ice for 10 minutes and treated with pulse at the capacity of 1.5kV, 25µFD. After recovering for 10 minutes at a room temperature the electroporated cells were added to CHO-S-SFM II (GIBCO BRL) containing 10% bovine fetal serum and cultivated. After cultivating for 2 days the cultivation was continued in CHO-S-SFM II (GIBCO BRL) containing 5nM methotrexate (SIGMA) and 10% bovine fetal serum. From thus obtained clones a clone with high expression rate was selected as the production cell line for 12B5 single chain Fv. After cultivating in serum-free medium CHO-S-SFM II (GIBCO BRL) containing 5nM methotrexate (SIGMA), the culture supernatant was obtained by centrifugal separation of cell debris.

#### 7.5 Purification of single chain Fv derived from 12B5 produced by CHO cells

[0238] The culture supernatant of CHO cell line expressing 12B5 single chain Fv obtained in 7.4 was purified by anti-FLAG antibody column and gel filtration column.

##### (1) Anti-FLAG antibody column

[0239] The culture supernatant was added to anti-FLAG M2 affinity gel (SIGMA) equilibrated by PBS. After washing the column by the same buffer the proteins adsorbed to the column were eluted by 0.1M glycine-HCl buffer (pH 3.5). The eluted fractions were immediately neutralized by adding 1M Tris-HCl buffer (pH 8.0). The eluted fractions were analyzed by SDS-PAGE and the fraction which was confirmed to contain the single chain Fv was concentrated using Centricon-10 (MILLIPORE).

(2) Gel filtration

**[0240]** The concentrated solution obtained in (1) was added to Superdex200 column (10x300mm, AMERSHAM PHARMACIA) equilibrated by PBS containing 0.01% Tween20. The product sc12B5 was eluted in two peaks (A, B) (see Fig. 48). The fractions A and B were analyzed using the 14%-SDS-polyacrylamide gel. The sample was processed by electrophoresis in the presence and absence of a reducing agent according to Laemmli method, and stained by Coomassie Brilliant Blue after the electrophoresis. As shown in Fig. 49 the fractions A and B, regardless of the presence of the reducing agent or its absence, produced a single band having an apparent molecular weight of about 31 kD. When the fractions A and B were analyzed by gel filtration using Superdex200 PC 3.2/30 (3.2x300mm, AMERSHAM PHARMACIA), the fraction A produced an eluted product at an apparent molecular weight of about 44 kD and the fraction B produced at 22kD (see Fig. 50a and b). The results show that the fraction A is the non-covalent bond dimer of sc12B5 single chain Fv, and B is the monomer.

7.6 Measurement of TPO-like agonist activity of various single chain Fvs

**[0241]** The TPO-like activity of anti-MPL single chain antibody was evaluated by measuring the proliferation activity to BaF/3 cells (BaF/mpl) expressing human TPO receptor (MPL). After washing BaF/Mpl cells two times by RPMI1640 culture medium (GIBCO) containing 10% bovine fetal serum (GIBCO), the cells were suspended in the culture medium at cell density of  $5 \times 10^5$  cells/ml. The anti-MPL single chain antibody and human TPO (R&D Systems) was diluted with the culture medium, respectively. 50 $\mu$ l of the cell suspension and 50 $\mu$ l of the diluted antibody or human TPO were added in 96-well microplate (flat bottom) (Falcon), and cultivated in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 24 hours. After the incubation 10 $\mu$ l of WST-8 reagent (reagent for measuring the number of raw cells SF: Nacalai Tesque) was added and the absorbance was immediately measured at measurement wavelength of 450nm and at reference wavelength of 620nm using fluorescence absorbency photometer SPECTRA Fluor (TECAN). After incubating in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 2 hours, the absorbance at 450nm of measurement wavelength and 620nm of reference wavelength was again measured using SPECTRA Fluor. Since WST-8 reagent developed the color reaction depending upon the number of live cells at wavelength of 450nm, the proliferation activity of BaF/Mpl based on the change of absorbance in 2 hours was evaluated by ED 50 calculated as follows. In the proliferation reaction curve wherein the absorbance was plotted on the ordinate against the antibody concentration on the abscissa, the absorbance at the plateau was set 100% reaction rate. Obtaining an approximation formula by straight line approximation method based on the plotted values close to 50% reaction rate, the antibody concentration of 50% reaction rate was calculated and adopted as ED 50.

**[0242]** The results of the agonist activity to MPL measured by using culture supernatants of COS-7 cells expressing various 12B5 antibody molecules showed as illustrated in Fig. 51 that 12B5IgG having bivalent antigen-binding site increased the absorbance in concentration-dependent manner and had TPO-like agonist activity (ED50; 29nM), while the agonist activity of 12B5Fab having monovalent antigen-binding site was very weak (ED50; 34,724nM). On the contrary the single chain Fv (sc12B5) having monovalent antigen-binding site like Fab showed strong agonist activity at a level that ED50 was 75nM. However it has been known that variable regions of H chain and L chain of the single chain Fv are associated through non-covalent bond and, therefore, each variable region is dissociated in a solution and can be associated with variable region of other molecule to form multimers like dimers. When the molecular weight of sc12B5 purified by gel filtration was measured, it was confirmed that there were molecules recognized to be monomer and dimer (see Fig. 48). Then monomer sc12B5 and dimer sc12B5 were isolated (see Fig. 50) and measured for the agonist activity to MPL. As shown in Figs. 51 and 52, ED50 of sc12B5 monomer was 4438.7nM, which confirmed that the agonist activity was reduced compared with the result using culture supernatant of COS-7 cells. On the contrary single chain Fv (sc12B5 dimer) having bivalent antigen-binding site showed about 400-fold stronger agonist activity (ED50; 10.1nM) compared with monovalent sc12B5. Furthermore, the bivalent single chain Fv showed the agonist activity equivalent to or higher than the agonist activity of human TPO and 12B5IgG.

## Example 8

Construction of a gene encoding the variable region of human antibody 12E10 against human MPL

**[0243]** A DNA encoding variable region of human monoclonal antibody 12E10 against human MPL was constructed as follows:

8.1 Construction of a gene encoding 12E10 H chain V region

**[0244]** The nucleotide sequence SEQ ID NO:86 was designed as a gene encoding H chain V region of human antibody 12E10 binding to human MPL on the basis of the amino acid sequence described in WO99/10494 (SEQ ID NO:85). The

full length of nucleotide sequence was designed by connecting to its 5'-end the leader sequence (SEQ ID NO:87) derived from human antibody gene (GenBank accession No. AF062252). The designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12E10VH1, 12E10VH2, 12E10VH3, 12E10VH4). 12E10VH1 (SEQ ID NO: 88) and 12E10VH3 (SEQ ID NO: 90) were synthesized in the sense direction; and 12E10VH2 (SEQ ID NO: 89) and 12E10VH4 (SEQ ID NO: 91) in the antisense direction, respectively. After assembling each synthesized oligonucleotide by respective complementarity, the external primers (12E10VHS and 12E10VHA) were added to amplify the full length of the gene. 12E10VHS (SEQ ID NO: 92) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have Hind III restriction enzyme recognition site and Kozak sequence, and 12E10VHA (SEQ ID NO: 93) was designed to hybridize to the nucleotide sequence encoding C-terminal of H chain V region by the reverse primer and to have a splice donor sequence and BamHI restriction enzyme recognition site, respectively.

**[0245]** 100  $\mu$ l of the PCR solution containing 10  $\mu$ l of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs (dATP, dGTP, dCTP, dTTP), 5 units of DNA-polymerase AmpliTaq Gold (all by PERKIN ELMER) and each 2.5pmole of each synthesized oligonucleotide (12E10VH-1 to -4) was heated at 94°C of the initial temperature for 9 minutes, at 94°C for 2 minutes, at 55°C for 2 minutes and 72°C for 2 minutes. After repeating the cycle two times each 100 pmole of external primer 12E10VHS and 12E10VHA were added. The mixture was subjected to the cycle consisting of at 94°C for 30 seconds, at 55°C for 30 seconds and 72°C for 1 minute 35 times and heated at 72°C for further 5 minutes.

**[0246]** The PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes BamHI and Hind III, and cloned into a human H chain expression vector HEF-gy1. After determining the DNA sequence the plasmid containing the correct DNA sequence was named HEF-12E10H-gy1.

**[0247]** The HEF-12E10H-gy1 was digested by restriction enzymes EcoRI and BamHI to produce the gene encoding 12E10VH and then cloned into a human Fab H chain expression vector pCOS-Fd to produce pFd-12E10H. The human Fab H chain expression vector was constructed by amplifying the DNA (SEQ ID NO: 63) containing the intron region existing between the genes encoding human antibody H chain V region and the constant region, and the gene encoding a part of the human H chain constant region by PCR, and inserting the PCR product into animal cell expression vector pCOS1. The human H chain constant region was amplified for the gene under the same conditions mentioned above using as the template HEF-gyl, as the forward primer G1CH1-S (SEQ ID NO: 64) which was designed to hybridize to 5'-end sequence of intron 1 and to have restriction enzyme recognition sites EcoRI and BamHI and as the reverse-primer G1CHL-A (SEQ ID NO: 65) which was designed to hybridize to 3'-end DNA of human H chain constant region CH1 domain and to have a sequence encoding a part of hinge region, two stop codons and restriction enzyme recognition site Bgl II.

**[0248]** The nucleotide sequence and amino acid sequence of the reconstructed 12E10 H chain variable region which were included in plasmids HEF-12E10H-gy1 and pFd-12E10H are shown in SEQ ID NO: 94.

## 8.2 Construction of a gene encoding 12E10 L chain V region

**[0249]** The nucleotide sequence SEQ ID NO:96 was designed as a gene encoding L chain V region of human antibody 12E10 binding to human MPL on the basis of the amino acid sequence described in WO99/10494 (SEQ ID NO:95). It was further designed by connecting to its 5'-end the leader sequence (SEQ ID NO: 97) derived from human antibody gene (Mol. Immunol. 1992; 29: 1515-1518). In the same way as mentioned above the designed nucleotide sequence was divided into four oligonucleotides having overlapping sequences of 15 bp each (12E10VL1, 12E10VL2, 12E10VL3, 12E10VL4) and synthesized respectively. 12E10VL1 (SEQ ID NO: 98) and 12E10VL3 (SEQ ID NO: 100) had sense sequences, and 12E10VL2 (SEQ ID NO: 99) and 12E10VL4 (SEQ ID NO: 101) had antisense sequences, respectively. Each of the synthesized oligonucleotides was assembled by respective complementarity and mixed with the external primers (12E10VLS and 12E10VLA) to amplify the full length of the gene. 12E10VLS (SEQ ID NO: 102) was designed to hybridize to 5'-end of the leader sequence by the forward primer and to have EcoRI restriction enzyme recognition site and Kozak sequence. 12E10VLA (SEQ ID NO: 103) was designed to hybridize to the nucleotide sequence encoding C-terminal of L chain V region by the reverse primer and to have a BlnI restriction enzyme recognition site.

**[0250]** Performing the PCR as mentioned above, the PCR product was purified by 1.5% low-melting-temperature agarose gel (Sigma), digested by restriction enzymes EcoRI and BlnI, and cloned into pUC19 containing a gene for human lambda chain constant region. After determining the DNA sequence the plasmid containing the correct DNA sequence was digested by EcoRI to produce a gene encoding 12E10 L chain V region and human lambda chain constant region and then inserted in expression vector pCOS1. The plasmid having 12E10 L chain gene (SEQ ID NO: 104) was named pCOS-12E10L.

## 8.3 Production of reconstructed 12E10 single chain Fv

**[0251]** The reconstructed 12E10 antibody single, chain Fv was designed to be in the order of 12E10VH-linker-12E10VL

and to have FLAG sequence (SEQ ID NO: 105) at C-terminal to facilitate the detection and purification. The reconstructed 12E10 chain Fvs (sc12E10 and db12E10) were constructed using a linker sequence consisting of 15 amino acids represented by (Gly<sub>4</sub>Ser)<sub>3</sub> or 5 amino acids represented by (Gly<sub>4</sub>Ser)<sub>1</sub>. (1) Production of the reconstructed 12E10 single chain Fv using the linker sequence consisting of 5 amino acids

**[0252]** The gene encoding the reconstructed 12E10 single chain Fv, which contained the linker sequence consisting of 5 amino acids, was constructed by introducing the nucleotide sequence for the linker (Gly<sub>4</sub>Ser)<sub>1</sub> to 3'-end of the gene encoding 12E10 H chain V region and to 5'-end of the gene encoding 12E10 L chain V region, amplifying thus obtained respective gene by PCR and connecting the amplified genes. Four PCR primers (A-D) were used to produce the reconstructed 12E10 single chain Fv. Primers A and C had sense sequences, and primers B and D had antisense sequences.

**[0253]** The forward primer for H chain V region was 12E10S (Primer A, SEQ ID NO: 106). The reverse primer DB2 (Primer B, SEQ ID NO: 107) for H chain V region was designed to hybridize to DNA encoding C-terminal of H chain V region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>1</sub> and the nucleotide sequence encoding N-terminal of L chain V region.

**[0254]** The forward primer DB1 (Primer C, SEQ ID NO: 108) for L chain V region was designed to hybridize to DNA encoding the N-terminal of L chain V region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>1</sub> and the nucleotide sequence encoding C-terminal of H chain V region. The reverse primer 12E10FA (Primer D, SEQ ID NO: 109) for L chain V region was designed to hybridize to DNA encoding the C-terminal of L chain V region and to have the nucleotide sequence encoding FLAG and NotI restriction enzyme recognition site.

**[0255]** In the first PCR step, two reactions A-B and C-D were performed, and the two PCR products obtained from the first step PCR were assembled by respective complementarity. After adding primers A and D the full length DNA encoding the reconstructed 12E10 single chain Fv having the linker consisting of 5 amino acids was amplified (the second PCR). In the first step PCR, the plasmid HEF-12E10H-gy1 (see Example 8.2) encoding the reconstructed 12E10 H chain V region and pCOS-12E10L (see Example 8.1) encoding the reconstructed 12E10 L chain V region were used as templates, respectively.

**[0256]** 50μl of the first step PCR solution contained 5μl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs, 5 units of DNA polymerase AmpliTaq Gold (by PERKIN ELMER), each 100 pmole of each primer and 100ng of each template DNA. The PCR solution was heated at 94°C of the initial temperature for 9 minutes, at 94 for 30 seconds, 55°C for 30 seconds and 72°C for 1 minute. After repeating the cycle 35 times the reaction mixture was further heated at 72°C for 5 minutes.

**[0257]** The PCR products A-B (429bp) and C-D (395bp) were assembled by the second PCR. The second step PCR mixture solution (98μl) containing 1μl each of the first PCR product A-B and C-D as templates, 100 pmole each of each primer, 10μl of 10 x PCR Gold Buffer II, 1.5mM MgCl<sub>2</sub>, 0.08mM dNTPs and 5 units of DNA polymerase AmpliTaq Gold (by PERKIN ELMER) was reacted under the same conditions as mentioned above.

**[0258]** The DNA fragment of 795bp produced by the second PCR was purified using 1.5% low-melting-temperature agarose gel, digested by EcoRI and NotI, and cloned into pCHO1 vector or pCOS1 vector. The expression vector pCHO1 was a vector constructed by deleting the antibody gene from DHFR-ΔE-RVH-PM1-f (see WO92/19759) by EcoRI and SmaI digestion, and connecting to EcoRI-NotI-BamHI Adaptor (TAKARA SHUZO). After determining the DNA sequence the plasmids containing the DNA fragment encoding the correct amino acid sequence of reconstructed 12E10 single chain Fv were named pCHO-db12E10 and pCOS-db12E10. The nucleotide sequence and amino acid sequence of the reconstructed 12E10 single chain Fv included in the plasmids pCHO-db12E10 and pCOS-db12E10 are shown in SEQ ID NO: 110.

(2) Production of the reconstructed 12E10 single chain Fv using the linker sequence consisting of 15 amino acids

**[0259]** The gene encoding the reconstructed 12E10 antibody single chain Fv, which contained the linker sequence consisting of 15 amino acids, was constructed by introducing the nucleotide sequence for the linker (Gly<sub>4</sub>Ser)<sub>3</sub> to 3'-end of the gene encoding 12E10 H chain V region and to 5'-end of the gene encoding 12E10 L chain V region, amplifying thus obtained respective gene by PCR and connecting the amplified genes. Four PCR primers (A-D) were used for production of the reconstructed 12E10 single chain Fv. Primers A and C had sense sequences, and primers B and D had antisense sequences.

**[0260]** The forward primer for H chain V region was 12E10S (Primer A, SEQ ID NO: 106). The reverse primer sc4.3 (Primer B, SEQ ID NO: 111) for H chain V region was designed to hybridize to DNA encoding C-terminal of H chain V region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>3</sub> and the nucleotide sequence encoding N-terminal of L chain V region.

**[0261]** The forward primer scl.3 (Primer C, SEQ ID NO: 112) for L chain V region was designed to hybridize to DNA encoding the N-terminal of L chain V region and to have the nucleotide sequence encoding the linker (Gly<sub>4</sub>Ser)<sub>3</sub> and the nucleotide sequence encoding C-terminal of H chain V region. The reverse primer 12E10FA (Primer D, SEQ ID NO: 109) for L chain V region was designed to hybridize to DNA encoding the C-terminal of L chain V region and to have

the nucleotide sequence encoding FLAG and NotI restriction enzyme recognition site.

**[0262]** In the first PCR step, two reactions A-B and C-D were performed, and the two PCR products obtained from the first step PCR were assembled by respective complementarity. After adding primers A and D the full length DNA encoding the reconstructed 12E10 single chain Fv having the linker consisting of 15 amino acids was amplified (the second PCR). In the first step PCR, the plasmid pCOS-db12E10 (see Example 8.3(1)) encoding the reconstructed 12E10 single chain Fv was used as template.

**[0263]** 50 $\mu$ l of the first step PCR solution contained 5 $\mu$ l of 10 x ExTaq Buffer, 0.4mM dNTPs, 2.5 units of DNA polymerase TaKaRa ExTaq (by TAKARA), each 100 pmole of each primer and 10ng of each template DNA. The PCR solution was heated at 94°C of the initial temperature for 30 seconds, at 94 for 15 seconds and 72°C for 2 minute, and the cycle was repeated 5 times. After repeating 28 times the -cycle of at 94°C for 15 seconds and at 70°C for 2 minutes, the reaction mixture was further heated at 72°C for 5 minutes.

**[0264]** The PCR products A-B (477bp) and C-D (447bp) were assembled by the second PCR. The second step PCR mixture solution (98 $\mu$ l) containing 1 $\mu$ l each of the first PCR products A-B and C-D as templates, 100 pmole each of each primer A and D, 5 $\mu$ l of 10 x ExTaq Buffer, 0.4mM dNTPs, 2.5 units of DNA polymerase TaKaRa ExTaq (by TAKARA) was reacted under the same conditions as mentioned above.

**[0265]** The DNA fragment of 825bp produced by the second PCR was purified using 1.0% low-melting-temperature agarose gel, digested by EcoRI and NotI. Thus obtained DNA fragment was cloned into pCH01 vector or pCOS1 vector. After determining the DNA sequence the plasmids containing the DNA fragment encoding the correct amino acid sequence of reconstructed 12E10 single chain Fv were named pCHO-sc12E10 and pCOS-sc12E10. The nucleotide sequence and amino acid sequence of the reconstructed 12E10 single chain Fv included in the plasmids pCHO-sc12E10 and pCOS-sc12E10 are shown in SEQ ID NO: 113.

#### 8.4 Expression of antibody 12E10 (IgG, Fab) and single chain Fv polypeptide by animal cell

**[0266]** Antibody 12E10 (IgG, Fab) and single chain Fv derived from antibody 12E10 (linker sequence 5 amino acids, 15 amino acids) were expressed by using COS-7 cells or CHO cells.

**[0267]** The transient expression using COS-7 cells was performed as follows. The transfection was performed by electroporation method using Gene Pulser II equipment (BioRad). For the expression of antibody 12E10 (IgG) each 10 $\mu$ g of the above-mentioned expression vector HEF-12E10H-gy1 and pCOS-12E10L were added, for the expression of 12E10Fab fragment each 10 $\mu$ g of pFd-12E10H and pCOS-12E10L were added and for the expression of single chain Fv of pCOS-sc12E10 (10 $\mu$ g) or pCOS-db12E10 (10 $\mu$ g) was added to COS-7 cells ( $1 \times 10^7$  cells/ml) suspended in 0.8ml of PBS. The mixture kept in a cuvette was treated by pulse at the capacity of 1.5kV, 25 $\mu$ FD. After recovering for 10 minutes in a room temperature the electroporated cells were added to DMEM medium (GIBCO BRL) containing 10% bovine fetal serum and cultivated. After cultivating overnight the cells were washed once by PBS, added to serum-free medium CHO-S-SFM II (GIBCO BRL) and cultivated for 3 days. The culture supernatant was centrifuged to remove cell debris and filtered with 0.22 $\mu$ m filter.

**[0268]** To establish a stable expression CHO cell line for the single chain Fv (polypeptide) derived from antibody 12E10, the expression vector pCHO-sc12E10 or pCHO-ds12E10 was introduced into CHO cells respectively.

**[0269]** Each expression vector was introduced into CHO cells by electroporation method using Gene Pulser II equipment (BioRad). Linearized DNA (100 $\mu$ g) obtained by digestion with restriction enzyme PvuI and CHO cells ( $1 \times 10^7$  cells/ml) suspended in 0.8 ml of PBS were mixed in a cuvette, left stationary on ice for 10 minutes and treated with pulse at the capacity of 1.5kV, 25 $\mu$ FD. After recovering for 10 minutes at a room temperature the electroporated cells were added to CHO-S-SFM II medium (GIBCO BRL) containing 10% dialyzed bovine fetal serum and nucleic acid and cultivated. After cultivating for 2 days the cultivation was continued in nucleic acid-free CHO-S-SFM II medium (GIBCO BRL) containing 10% dialyzed bovine fetal serum. From thus obtained clones a clone with high expression rate was selected as the production cell line for 12E10 single chain Fv. After cultivating in serum-free CHO-S-SFM II medium (GIBCO BRL), the culture supernatant was centrifuged to remove cell debris and filtered with 0.22 $\mu$ m filter.

#### 8.5 Purification of single chain Fv derived from 12E10. produced by CHO cells

**[0270]** The culture supernatants produced by CHO cell lines expressing 12E10 single chain Fvs (sc12E10, db12E10) obtained in Example 8.4 were purified by anti-FLAG antibody column and gel filtration column respectively to produce purified single chain Fvs.

##### (1) Purification with anti-FLAG antibody column

**[0271]** Each culture supernatant (sc12E10, db12E10) was added to anti-FLAG M2 affinity gel column (SIGMA) equilibrated by 50mM Tris-HCl buffer (pH7.4) containing 150mM NaCl. After washing the column by the same buffer the



proteins adsorbed to the column were eluted by 100mM glycine buffer (pH 3.5). The eluted fractions were immediately neutralized by adding 1M Tris-HCl buffer (pH 8.0) and analyzed by SDS-PAGE. The fraction which was confirmed to contain the single chain Fv was pooled and concentrated about 20-fold using Centricon-10 (AMICON).

## (2) Gel filtration

**[0272]** The concentrated solution obtained in (1) was added to Superdex200 column HR (10x300mm, AMERSHAM PHARMACIA) equilibrated by PBS containing 0.01% Tween20. Chromatograms were shown in Fig. 53 and 54. The product sc12E10 was eluted in two peaks (A, B) (see Fig. 53). The product db12E10 was eluted in two peaks (C, D) (see Fig. 54). Each peak fraction was collected, treated in the presence and absence of a reducing agent, processed by electrophoresis according to Laemmli method and stained by Coomassie Brilliant Blue after the electrophoresis. As shown in Fig. 55 the all of fractions A, B, C and D, regardless of the presence or absence of the reducing agent, produced a single band having an apparent molecular weight of about 31 kD. When these fractions were analyzed by gel filtration using Superdex200 HR, the fraction A produced a product eluted at an apparent molecular weight of About 42 kD, the fraction B at 20kD (see Fig. 56), fraction C at 69kD and fraction D at 41kD (see Fig. 57). The results suggest that sc12E10-derived fraction A is the non-covalent bond dimer of single chain Fv and the fraction B is the monomer of single chain Fv, and the db12E10-derived fraction C is the non-covalent bond trimer of single chain Fv and D is non-covalent bond dimer of single chain Fv.

## 8.6 Measurement of TPO-like agonist activity of various single chain Fvs

**[0273]** The TPO-like activity of anti-mpl single chain antibody was evaluated by measuring the proliferation activity to Ba/F3 cells (BaF/mpl) expressing human TPO receptor (MPL).

**[0274]** After washing BaF/mpl cells two times by RPMI1640 medium (GIBCO) containing 1% bovine fetal serum (GIBCO), the cells were suspended in the medium at cell density of  $5 \times 10^5$  cells/mL. The anti-MPL single chain antibody or human TPO (R&D Systems) was diluted with the medium, respectively. 50 $\mu$ l of the cell suspension and 50 $\mu$ l of the diluted antibody or human TPO were added in 96-well microplate (flat bottom) (Corning), and cultivated in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 24 hours. After the incubation 10 $\mu$ l of WST-8 reagent (reagent for measuring the number of raw cells SF: Nacalai Tesque) was added and the absorbance was immediately measured at measurement wavelength of 450nm and at reference wavelength of 655nm using absorbency photometer Benchmark Plus (BioRad). After incubating in CO<sub>2</sub> incubator (CO<sub>2</sub> concentration: 5%) for 2 hours, the absorbance at 450nm of measurement wavelength and 655nm of reference wavelength was again measured using Benchmark Plus. Since WST-8 reagent developed the color reaction depending upon the number of live cells at wavelength of 450nm, the proliferation activity of BaF/mpl was evaluated based on the change of absorbance in 2 hours.

**[0275]** The agonist activity to MPL measured by using culture supernatants of COS-7 cells expressing various 12E10 antibody molecules are shown in Fig. 58. Single chain Fvs having the 5-amino-acid-linker (ds12E10) and the 15-amino-acid-linker (sc12E10) increased the absorbance in concentration-dependent manner, showing TPO-like, agonist activity (ED50; 9pM and 51pM respectively), while 12E10IgG and 12E10Fab had no activity.

**[0276]** It has been known that H chain and L chain of the single chain Fv are associated not only within a molecule but also between molecules to form multimers such as dimer. When the culture supernatants of CHO cells expressing single chain Fvs of 12E10 were gel filtrated and tested for agonist activity on MPL. The results were shown in Fig. 59. The dimer, which was contained in sc12E10 in a small amount, showed about 5000-fold stronger TPO-like agonist activity (sc12E10 dimer, ED50; 1.9pM) compared with the monomer (sc12E10 monomer, ED50; >10nM). The activity was higher than that of TPO (ED50; 27pM). The dimer of db12E10 (db12E10 dimer, ED50; 2.0pM) showed strong activity comparable to that of sc12E10 dimer. db12E10 trimer (ED50; 7.4pM), which was presumed to be a trimer from molecular weight obtained by gel filtration, showed a high activity which is lower than that of db12E10 dimer. Those results suggest that it is important for the activity of agonist antibody 12E10 that the antigen-binding site is bivalent (dimer). Considering the fact that 12E10 IgG had no activity, other factors than being bivalent are presumed to be important such as the location of antigen-binding site, the distance or the angle.

## EXPLANATION OF DRAWINGS

### [0277]

Fig. 1 shows the result of flow cytometry, illustrating that human IgG antibody does not bind to L1210 cells expressing human IAP (hIAP/L1210).

Fig. 2 shows the result of flow cytometry, illustrating that the chimera MABL-1 antibody specifically binds to L1210 cells expressing human IAP (hIAP/L1210).

Fig. 3 shows the result of flow cytometry, illustrating that the chimera MABL-2 antibody specifically binds to L1210 cells expressing human IAP (hIAP/L1210).

Fig. 4 schematically illustrates the process for producing the single chain Fv according to the present invention.

Fig. 5 illustrates a structure of an expression plasmid which can be used to express a DNA encoding the single chain Fv of the invention in *E. coli*.

Fig. 6 illustrates a structure of an expression plasmid which is used to express a DNA encoding the single chain Fv of the invention in mammalian cells.

Fig. 7 shows the result of western blotting in Example 5.4. From the left, a molecular weight marker (which indicates 97.4, 66, 45, 31, 21.5 and 14.5 kDa from the top), the culture supernatant of pCHO1-introduced COS7 cells and the culture supernatant of pCHOM2-introduced COS7 cells. It illustrates that the reconstructed single chain Fv of the antibody MABL-2 (arrow) is contained in the culture supernatant of the pCHOM2-introduced cells.

Fig. 8 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of pCHO1/COS7 cell as a control does not bind to pCOS1/L1210 cell as a control.

Fig. 9 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of MABL2-scFv/COS7 cells does not bind to pCOS1/L1210 cells as a control.

Fig. 10 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of pCOS1/COS7 cells as a control does not bind to hIAP/L1210 cells.

Fig. 11 shows the result of flow cytometry, illustrating that an antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically binds to hIAP/L1210 cells.

Fig. 12 shows the result of the competitive ELISA in Example 5.6, wherein the binding activity of the single chain Fv of the invention (MABL2-scFv) to the antigen is demonstrated in terms of the inhibition of binding of the mouse monoclonal antibody MABL-2 to the antigen as an index, in comparison with the culture supernatant of pCHO1/COS7 cells as a control.

Fig. 13 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce the apoptosis of pCOS1/L1210 cells as a control.

Fig. 14 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells does not induce apoptosis of pCOS1/L1210 cells as a control.

Fig. 15 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce apoptosis of hIAP/L1210 cells.

Fig. 16 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically induces apoptosis of hIAP/L1210 cells.

Fig. 17 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of pCHO1/COS7 cells as a control does not induce apoptosis of SCRF-CEM cells (at 50% of the final concentration).

Fig. 18 shows the results of the apoptosis-inducing effect in Example 5.7, illustrating that the antibody in the culture supernatant of MABL2-scFv/COS7 cells specifically induces apoptosis of CCRF-CEM cells (at 50% of the final concentration).

Fig. 19 shows the chromatogram obtained in the purification of the single chain Fv derived from the antibody MABL-2 produced by the CHO cells in Example 5.9, illustrating that fraction A and fraction B were obtained as the major peaks when the fraction from Blue-sepharose column was purified with hydroxyapatite column.

Fig. 20 shows the results of purification by gel filtration of fraction A and fraction-B obtained in Example 5.9-(2), illustrating that the major peaks (AI and BI, respectively) were eluted from fraction A at approximately 36 kD of the apparent molecular weight and from fraction B at approximately 76 kD.

Fig. 21 is the analysis on SDS-PAGE of the fractions obtained in the purification of the single chain Fv derived from the antibody MABL-2 produced by the CHO cells in Example 5.9, illustrating that a single band of approximately 35 kD of molecular weight was observed in both fractions.

Fig. 22 shows the results of analysis of fractions AI and BI obtained by gel filtration in the purification of the single chain Fv derived from the antibody MABL-2 produced by the CHO cells, wherein fraction AI comprises monomer and fraction BI comprises dimer.

Fig. 23 illustrates a structure of an expression plasmid which can be used to express a DNA encoding the single chain Fv of the invention in *E. coli*.

Fig. 24 shows the results of purification on the gel filtration column of crude products of the single chain Fv polypeptide derived from the antibody MABL-2 produced by *E. coli* obtained in Example 5.12, wherein each peak indicates monomer or dimer, respectively, of the single chain Fv produced by *E. coli*.

Fig. 25 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that mouse IgG antibody as a control does not induce apoptosis of hIAP/L1210 cells (the final concentration of 3  $\mu$ g/ml).

Fig. 26 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that the dimer of MABL2-scFv produced by the CHO cells remarkably induces apoptosis of hIAP/L1210 cells (the final concentration of 3  $\mu$ g/ml).

Fig. 27 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that the dimer of MABL2-scFv produced by *E. coli* remarkably induces apoptosis of hIAP/L1210 cells (the final concentration of 3  $\mu$ g/ml).

Fig. 28 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that apoptosis induction to hIAP/L1210 cells by the MABL2-scFv monomer produced by the CHO cells is the same level as that of the control (the final concentration of 3  $\mu$ g/ml).

Fig. 29 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that apoptosis induction to hIAP/L1210 cells of the MABL2-scFv monomer produced by *E. coli* is the same level as that of control (the final concentration of 3  $\mu$ g/ml).

Fig. 30 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that mouse IgG antibody used as a control does not induce apoptosis of hIAP/L1210 cells even when anti-FLAG antibody is added (the final concentration of 3  $\mu$ g/ml).

Fig. 31 shows the results of the apoptosis-inducing effect in Example 5.13, illustrating that MABL2-scFv monomer produced by the CHO cells remarkably induces apoptosis of hIAP/L1210 cells when anti-FLAG antibody is added (the final concentration of 3  $\mu$ g/ml).

Fig. 32 shows the results of quantitative measurement of human IgG in the serum of a human myeloma cell line KPMM2-transplanted mouse, indicating amounts of human IgG produced by the human myeloma cells in the mouse. It illustrates that the dimer of scFv/CHO remarkably inhibited growth of the KPMM2 cells.

Fig. 33 shows the survival time of the mouse after the transplantation of tumor, illustrating that the scFv/CHO dimer-administered group elongated remarkably the survival time.

Fig. 34 illustrates a structure of an expression plasmid which expresses a modified antibody [sc(Fv)<sub>2</sub>] comprising two H chain V regions and two L chain V regions derived from the antibody MABL-2.

Fig. 35 illustrates a structure of a plasmid which expresses a scFv (HL type) wherein the V regions are linked in the manner of [H chain]-[L chain] without a peptide linker.

Fig. 36 illustrates a structure of the HL-type polypeptide and amino acid sequences of peptide linkers.

Fig. 37 illustrates a structure of a plasmid which expresses a scFv (LH type) wherein the V regions are linked in the manner of [L chain]-[H chain] without a peptide linker.

Fig. 38 illustrates a structure of the LH-type polypeptide and amino acid sequences of peptide linkers.

Fig. 39 shows the results of the western blotting in Example 6.4, illustrating that the modified antibody sc(Fv)<sub>2</sub> comprising two H chain V regions and two L chain V regions, and the MABL2-scFv having peptide linkers with different length are expressed.

Figs. 40a and 40b show the results of flow cytometry using the culture supernatant of COS7 cells prepared in Example 6.3 (1), illustrating that the MABL2-scFv and sc(Fv)<sub>2</sub> having peptide linkers with different length have high affinities against human IAP.

Fig. 41a and 41b show the results of the apoptosis-inducing effect in Example 6.6, illustrating that the scFv <HL3, 4, 6, 7, LH3, 4, 6 and 7> and the sc(Fv)<sub>2</sub> remarkably induce cell death of hIAP/L1210 cells.

Fig. 42 shows the results of the evaluation of antigen binding capacity in Example 6.10, illustrating that the dimer of scFv <HL5> and sc(Fv)<sub>2</sub> have high affinities against human IAP.

Fig. 43 shows the results of the *in vitro* apoptosis-inducing effect in Example 6.11, illustrating that the dimer of scFv <HL5> and the sc(Fv)<sub>2</sub> induce apoptosis of hIAP/L1210 cells and CCRF-CEM cells in concentration-dependent manner.

Fig. 44 shows the results of the quantitative measurement of M protein produced by a human myeloma cell line KPMM2 in the serum of the human myeloma cell-transplanted mouse. It illustrates that the dimer of scFv <HL5> and the sc(Fv)<sub>2</sub> remarkably inhibited growth of the KPMM2 cells.

Fig. 45 shows the survival time (days) of mice after the transplantation of tumor, illustrating that the survival time of the scFv <HL5> administrated-group was remarkably prolonged.

Fig. 46 shows the survival time (days) of mice after the transplantation of tumor, illustrating that the survival time of the sc(Fv)<sub>2</sub> administrated-group was remarkably prolonged.

Fig. 47 is a scheme showing the method for constructing DNA fragment encoding the reconstructed 12B5 single chain Fv containing the linker sequence consisting of 15 amino acids and the structure thereof.

Fig. 48 shows the purification result of each 12B5 single chain Fv by gel filtration obtained in Example 7.5 (1), illustrating that sc12B5 was divided into two peaks (fractions A and B).

Fig. 49 shows the analytical result of each fraction A and B by SDS-PAGE performed in Example 7.5 (2).

Fig. 50 shows the analytical result of each fraction A and B by Superdex200 column performed in Example 7.5 (2), illustrating that the major peak of fraction A was eluted at an apparent molecular weight of about 44 kD shown in (a) and that the major peak of fraction B was eluted at an apparent molecular weight of about 22kD shown in (b).

Fig. 51 shows the measurement result of the TPO-like agonist activity of sc12B5 and antibody 12B5 (IgG, Fab), illustrating that 12B5IgG and monovalent single chain Fv (sc12B5) showed TPO-like agonist activity in concentration-dependent manner.

Fig. 52 shows the measurement result of TOP-like agonist activity of sc12B5 monomer and dimer, illustrating that single chain Fv (sc12B5 dimer) having bivalent antigen-binding site had agonist activity about 400-fold higher than monovalent sc12B5 and that the efficacy is equivalent to or higher than human TPO.

Fig. 53 shows the purification result of obtained sc12E10 single chain antibody by gel filtration chromatography using Superdex200HR column, illustrating that Sc12E10 was divided into two peaks (fractions A and B).

Fig. 54 shows the purification result of obtained db12E10 single chain antibody by gel filtration chromatography using Superdex200HR column, illustrating that db12E10 was divided into two peaks (fractions C and D).

Fig. 55 shows SDS-PAGE analysis of fractions A and B (sc12E10) and fractions C and D (db12E10) under the reductive or non-reductive condition.

Fig. 56 shows the analytical result of fractions A and B by gel filtration chromatography using Superdex200HR column, illustrating (1) the major peak of fraction A was eluted at an apparent molecular weight of about 42 kD and (2) the major peak of fraction B was eluted at an apparent molecular weight of about 20kD.

Fig. 57 shows the analytical result of fractions C and D by gel filtration chromatography using Superdex200HR column, illustrating (1) the major peak of fraction C was eluted at an apparent molecular weight of about 69 kD and (2) the major peak of fraction D was eluted at an apparent molecular weight of about 41kD.

Fig. 58 is a graph showing the agonist activity of various 12E10 antibody molecules on MPL, illustrating that single chain Fvs (sc12E10, db12E10) showed TPO-like agonist activity while 12E10 IgG and 12E10 Fab did not.

Fig. 59 is a graph showing the agonist activity of monomer and dimer of sc12E10 and dimer and trimer of db12E10 on MPL, illustrating that dimer of sc12E10 and dimer and trimer of db12E10 showed higher TPO-like agonist activity than TPO.

## INDUSTRIAL APPLICABILITY

**[0278]** The modified antibodies of the invention have an agonist action capable of transducing a signal into cells by crosslinking a cell surface molecule(s) and are advantageous in that the permeability to tissues and tumors is high due to the lowered molecular size compared with antibody molecule (whole IgG). This invention provides the modified antibodies with an agonist activity remarkably higher than TPO or parent antibodies (whole IgG). Especially even parent antibodies without agonist activity can be altered into the modified antibodies with an agonist activity higher than TPO. Therefore the modified antibodies can be used as signal-transducing agonists. The modification of antibody molecule results in the reduction of side effects caused by intercellular crosslinking and provides novel medicines inducing only required action by crosslinking a cell surface molecule(s). Medical preparations containing as active ingredient the modified antibodies of the invention are useful as preventives and/or remedies for platelet-related-blood diseases, thrombocytopenia caused by chemotherapy for cancers or leukemia and the like.

## SEQUENCE LISTING

### [0279]

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<120> Degraded TPO Agonist Antibody

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EP 1 327 680 B1

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EP 1 327 680 B1

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100 105 110

15 tac tac tgt gca aga ggg ggt tac tat agt tac gac gac tgg ggc caa 384  
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln

115 120 125

20 ggc acc act ctc aca gtc tcc tca g 409  
 Gly Thr Thr Leu Thr Val Ser Ser

130 135

25 <210> 7  
 <211> 394  
 <212> DNA  
 <213> Mus

30 <220>  
 <221> CDS  
 <222> (1)... (393)  
 <223> pGEM-M2L. 1-57;signal peptide, 58-394;mature peptide

35 <400> 7

40 atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct ggt 48  
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly

1 5 10 15

45 tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc 96  
 Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val

20 25 30

50

55



	agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt	144
5	Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu	
	35 40 45	
	gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag cca	192
10	Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro	
	50 55 60	
	ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct	240
15	Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser	
	65 70 75 80	
	ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca	288
20	Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr	
	85 90 95	
	ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc	336
25	Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys	
	100 105 110	
	tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg	384
30	Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu	
	115 120 125	
	gaa ata aaa c	394
	Glu Ile Lys	
40	130	

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu

35

40

45

gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag cca 192

Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro

50

55

60

ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser

65

70

75

80

ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca 288

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr

85

90

95

ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc 336

Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys

100

105

110

tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg 384

Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu

115

120

125

**gaa ata aaa c**

394

**Glu Ile Lys**

130

<210> 8

<211> 409

<212> DNA

<213> Mus

 $\langle 220 \rangle$ 

<221> CDS

<222> (1)... (408)

<223> pGEM-M2H. 1-57;signal peptide, 58-409;mature peptide

<400> 8

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 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly  
 5 1 5 10 15  
 gtc cac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96  
 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
 10 20 25 30  
 cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144  
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 15 35 40 45  
 gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192  
 Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu  
 20 50 55 60  
 gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240  
 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
 25 65 70 75 80  
 gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288  
 Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr  
 30 85 90 95  
 aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc 336  
 Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val  
 40 100 105 110  
 tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 384  
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln  
 45 115 120 125  
 ggc acc act ctc aca gtc tcc tca g 409  
 50  
 Gly Thr Thr Leu Thr Val Ser Ser  
 55 130 135

EP 1 327 680 B1

<210> 9  
 <211> 32  
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 <213> Artificial Sequence  
 5  
 <220>  
 <223> PCR primer  
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 10 cccaagcttc caccatgaag ttgcctgtta gg 32  
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 <211> 32  
 <212> DNA  
 15 <213> Artificial Sequence  
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 <223> PCR primer  
 20 <400> 10  
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 <211> 34  
 25 <212> DNA  
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 <220>  
 <223> PCR primer  
 30 <400> 11  
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 <211> 34  
 35 <212> DNA  
 <213> Artificial Sequence  
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 <223> PCR primer  
 40 <400> 12  
 cgcgcatcca ctcacctgag gagactgtga gagt 34  
 <210> 13  
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 <212> DNA  
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 45 <220>  
 <223> PCR primer  
 50 <400> 13  
 catgccatgg cgcaggtcca gctgcagcag 30  
 55 <210> 14  
 <211> 27  
 <212> DNA

EP 1 327 680 B1

<213> Artificial Sequence

<220>  
<223> PCR primer

5

<400> 14  
accaccacct gaggagactg tgagagt 27

<210> 15  
10 <211> 27  
<212> DNA  
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<220>  
15 <223> PCR primer

<400> 15  
gtctcctcag gtggtggtgg ttcgggt 27

20 <210> 16  
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<220>  
25 <223> PCR primer

<400> 16  
30 cacaacatcc gatccgccac caccoga 27

<210> 17  
<211> 27  
<212> DNA  
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35 <220>  
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<400> 17  
40 ggcggatcgg atgttgtgat gacccaa 27

<210> 18  
<211> 57  
<212> DNA  
45 <213> Artificial Sequence

<220>  
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50 <400> 18  
ccggaattct cattatttat cgtcatcgtc ttgtagtct ttatttcca gcttgg 57

<210> 19  
55 <211> 45  
<212> DNA  
<213> Artificial Sequence

<220>

**EP 1 327 680 B1**

<223> Linker amino acid sequence and nucleotide sequence

<400> 19

<sup>5</sup>

ggg ggt ggt ggt tgc ggt ggt ggt ggt tcg ggt ggt gcc gga tcg    45  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

<sup>10</sup>

                5                       10                            15

<210> 20

<211> 828

15 <212> DNA

<213> Mus

<220>

<221> CDS

20  $\langle 222 \rangle$  (1)... (822)

<223> pscM1. MABL1-scFv

<400> 20

25

30

35

40

45

50

55

atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc gct 48  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
 5           1                   5                   10                   15  
 gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga cct gac 96  
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Asp  
 10                   20                   25                   30  
 ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144  
 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
 15                   35                   40                   45  
 tac acc ttc gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg 192  
 Tyr Thr Phe Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly  
 20                   50                   55                   60  
 cag ggc ctt gag tgg att gga tat att tat cct tac aat gat ggt act 240  
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr  
 25                   65                   70                   75                   80  
 aag tac aat gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa 288  
 Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys  
 30                   85                   90                   95  
 tcc tcc agc gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac 336  
 Ser Ser Ser Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp  
 35                   100                   105                   110  
 tct gcg gtc tac tac tgt gca aga ggg ggt tac tat agt tac gac gac 384  
 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp  
 40                   115                   120                   125  
 tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg 432  
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser  
 45                   130                   135                   140  
 50  
 55

5 ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gat gtt gtg atg acc caa 480  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln  
 145 150 155 160  
 10 act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 528  
 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 165 170 175  
 15 tgc aga tct agt cag agc ctt cta cac agt aaa gga aac acc tat tta 576  
 Cys Arg Ser Ser Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu  
 180 185 190  
 20 caa tgg tac cta cag aag cca ggc cag tct cca aag ctc ctg atc tac 624  
 Gln Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr  
 25 195 200 205  
 aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt 672  
 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
 30 210 215 220  
 gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag 720  
 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu  
 35 225 230 235 240  
 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 768  
 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr  
 40 245 250 255  
 tcc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac 816  
 Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp  
 45 260 265 270  
 50 gat aaa taatga 828  
 Asp Lys

55 <210> 21  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

EP 1 327 680 B1

<220>

<223> PCR primer

<400> 21

5 acgcgtcgac tcccaggtcc agctgcagca g 31

<210> 22

<211> 18

<212> DNA .

10 <213> Artificial Sequence

<220>

<223> PCR primer

15 <400> 22

gaaggtgtat ccagaagc 18

<210> 23

<211> 819

20 <212> DNA

<213> Mus

<220>

<221> CDS

25 <222> (1)... (813)

<223> pCHOM1. MABL1-scFv

<400> 23

30 atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

35

40

45

50

55



1 5 10 15  
 5 gtc gac tcc cag gtc cag ctg cag cag tct gga cct gac ctg gta aag 96  
 Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys  
 20 25 30  
 10 cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144  
 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 15 gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg cag ggc ctt 192  
 Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu  
 50 55 60  
 20 gag tgg att gga tat att tat cct tac aat gat ggt act aag tac aat 240  
 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
 65 70 75 80  
 25 gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa tcc tcc agc 288  
 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser  
 85 90 95  
 30 gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac tct gcg gtc 336  
 Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val  
 100 105 110  
 35 tac tac tgt gca aga ggg ggt tac tat agt tac gac gac tgg ggc caa 384  
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln  
 115 120 125  
 40 ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tgc ggt ggt ggt 432  
 Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 130 135 140  
 45 ggt tgc ggt ggt ggc gga tgc gat gtt gtg atg acc caa act cca ctc 480  
 Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu  
 145 150 155 160  
 50  
 55

	tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct	528
5	Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser	
	165 170 175	
	agt cag agc ctt cta cac agt aaa gga aac acc tat tta caa tgg tac	576
10	Ser Gln Ser Leu Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr	
	180 185 190	
	cta cag aag cca ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc	624
15	Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser	
	195 200 205	
	aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg	672
20	Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly	
	210 215 220	
	aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga	720
25	Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly	
	225 230 235 240	
	gtt tat ttc tgc tct caa agt aca cat gti ccg tac acg tcc gga ggg	768
30	Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly Gly	
	245 250 255	
	ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat aaa taa	816
35	Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys	
	260 265 270	
40	tga	819

45           <210> 24  
              <211> 828  
              <212> DNA  
              <213> Mus

50           <220>  
              <221> CDS  
              <222> (1)... (822)  
              <223> pscM2. MABL2-scFv

55           <400> 24

atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta tta ctc gct 48  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
 5           1                   5                   10                   15  
 gcc caa cca gcc atg gcg cag gtc cag ctg cag cag tct gga cct gaa 96  
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu  
 10                   20                   25                   30  
 ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144  
 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
 15                   35                   40                   45  
 tac acc ttc gct aac cat gtt att cac tgg gtg aag cag aag cca ggg 192  
 Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly  
 20                   50                   55                   60  
 cag gcc ctt gag tgg att gga tat att tat cct tac aat gat ggt act 240  
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr  
 25                   65                   70                   75                   80  
 aag tat aat gag aag ttc aag gac aag gcc act ctg act tca gac aaa 288  
 Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys  
 30                   85                   90                   95  
 tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac 336  
 Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp  
 35                   100                   105                   110  
 tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac gac gac 384  
 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp  
 40                   115                   120                   125  
 45  
 50  
 55

tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tgc 432  
 5 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser  
 130 135 140  
 ggt ggt ggt ggt tgc ggt ggt ggc gga tgc gat gtt gtg atg acc caa 480  
 10 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln  
 145 150 155 160  
 agt cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 528  
 15 Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 165 170 175  
 tgc aga tca agt cag agc ctt gtg cac agt aat gga aag acc tat tta 576  
 20 Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr  
 180 185 190  
 cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac 624  
 25 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr  
 195 200 205  
 aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt 672  
 30 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
 210 215 220  
 gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct gag 720  
 35 Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu  
 225 230 235 240  
 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 768  
 40 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr  
 245 250 255  
 ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac 816  
 45 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp  
 260 265 270  
 .gat aaa taatga 828  
 55

**Asp Lys**

5

&lt;210&gt; 25

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Mus

10

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)... (813)

&lt;223&gt; pCHOM2. MABL2-scFv

15

&lt;400&gt; 25

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

25

gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96

Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys

20 25 30

30

cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

35

gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192

Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu

50 55 60

40

gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240

Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn

65 70 75 80

45

gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288

Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr

50

55

5                   85                   90                   95  
 aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc 336  
 Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val  
                   100                   105                   110  
 10   tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 384  
 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln  
                   115                   120                   125  
 15   ggc acc act ctc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt 432  
 Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 20   - 130                   135                   140  
 ggt tcg ggt ggt ggc gga tcg gat gtt gtg atg acc caa agt cca ctc 480  
 Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu  
 25   145                   150                   155                   160  
 tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca 528  
 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser  
 30                   165                   170                   175  
 agt cag agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac 576  
 Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr  
 35                   180                   185                   190  
 ctg cag aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc 624  
 Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser  
                   195                   200                   205  
 40   aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg 672  
 Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val  
                   210                   215                   220  
 45   aca gat ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga 720  
 Thr Asp Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly  
                   225                   230                   235                   240  
 50  
 55

gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg 768  
5 Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly  
245 250 255  
ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat aaa taa 816  
10 Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys  
260 265 270  
tga 819

20

<210> 26  
<211> 456  
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25

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<223> pCHO-shIAP. Soluble human IAP

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Met Trp Pro Leu Val Ala Ala Leu Leu Leu Gly Ser Ala Cys Cys Gly  
1 5 10 15

35 tca gct cag cta cta ttt aat aaa aca aaa tct gta gaa ttc acg ttt 96  
Ser Ala Gln Leu Leu Phe Asn Lys Thr Lys Ser Val Glu Phe Thr Phe  
20 25 30

40 tgt aat gac act gtc gtc att cca tgc ttt gtt act aat atg gag gca 144  
Cys Asn Asp Thr Val Val Ile Pro Cys Phe Val Thr Asn Met Glu Ala  
35 40 45

45 caa aac act act gaa gta tac gta aag tgg aaa ttt aaa gga aga gat 192  
Gln Asn Thr Thr Glu Val Tyr Val Lys Trp Lys Phe Lys Gly Arg Asp

50

55

50                      55                      60  
 5    att tac acc ttt gat gga gct cta aac aag tcc act gtc ccc act gac 240  
     Ile Tyr Thr Phe Asp Gly Ala Leu Asn Lys Ser Thr Val Pro Thr Asp  
 65                      70                      75                      80  
 10    ttt agt agt gca aaa att gaa gtc tca caa tta cta aaa gga gat gcc 288  
     Phe Ser Ser Ala Lys Ile Glu Val Ser Gln Leu Leu Lys Gly Asp Ala  
 85                      90                      95  
 15    tct ttg aag atg gat aag agt gat gct gtc tca cac aca gga aac tac 336  
     Ser Leu Lys Met Asp Lys Ser Asp Ala Val Ser His Thr Gly Asn Tyr  
 100                      105                      110  
 20    act tgt gaa gta aca gaa tta acc aga gaa ggt gaa acg atc atc gag 384  
     Thr Cys Glu Val Thr Glu Leu Thr Arg Glu Gly Glu Thr Ile Ile Glu  
 115                      120                      125  
 25    cta aaa tat cgt gtt gtt tca tgg ttt tct cca aat gaa aat gac tac 432  
     Leu Lys Tyr Arg Val Val Ser Trp Phe Ser Pro Asn Glu Asn Asp Tyr  
 130                      135                      140  
 30    aag gac gac gat gac aag tgatag 456  
     Lys Asp Asp Asp Asp Lys  
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 50    <210> 28  
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EP 1 327 680 B1

<400> 28  
ggaattctca ttattttatt tccagcttgg t 31

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Met Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly

gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc gct aac 96

Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn

cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg 144

His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp

att gga tat att tat cct tac aat gat ggt act aag tat aat gag aag 192  
 5 Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys  
 50 55 60  
 ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc 240  
 10 Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala  
 65 70 75 80  
 tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc tat tac 288  
 15 Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr  
 85 90 95  
 tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa ggc acc 336  
 20 Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr  
 100 105 110  
 act ctc aca gtc tcc tca ggt ggt ggt ggt tcc ggt ggt ggt ggt tcc 384  
 25 Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 115 120 125  
 ggt ggt ggc gga tcc gat gtt gtg atg acc caa agt cca ctc tcc ctg 432  
 30 Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu  
 130 135 140  
 cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag 480  
 35 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln  
 145 150 155 160  
 agc ctt gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag 528  
 40 Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln  
 165 170 175  
 aag cca ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga 576  
 45 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg  
 180 185 190  
 ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat 624  
 55

5           Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp  
               195                               200                               205  
           ttc aca ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat 672  
 10           Phe Thr Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr  
               210                               215                               220  
           ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc 720  
 15           Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr  
               225                               230                               235                               240  
           aag ctg gaa ata aaa taatga   741  
 20           Lys Leu Glu Ile Lys  
   245

25           <210> 30  
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 35           cagacagtgg tcaaaagt 18

              <210> 31  
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50           cgcgctcgacc gatccgccac caccogaacc accaccaccd gaaccaccac caccttttat 60  
               ttccagcttg gt   72

55           <210> 32  
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EP 1 327 680 B1

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<223> pCHOM2(Fv)2. MABL2-sc(Fv)2

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1 5 10 15  
15 gtc gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96  
Val Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
20 25 30  
20 cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144  
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
25 gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192  
Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu  
50 55 60  
30 gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240  
Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn  
65 70 75 80  
35 gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288

40

45

50

55

	Glu	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ser	Asp	Lys	Ser	Ser	Thr	
5						85					90					95	
	aca	gcc	tac	atg	gac	ctc	agc	agc	ctg	gcc	tct	gag	gac	tct	gcg	gtc	336
	Thr	Ala	Tyr	Met	Asp	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val	
10						100					105					110	
	tat	tac	tgt	gca	aga	ggg	ggg	tac	tat	act	tac	gac	gac	tgg	ggc	caa	384
	Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Tyr	Tyr	Thr	Tyr	Asp	Asp	Trp	Gly	Gln	
15						115					120					125	
	ggc	acc	act	ctc	aca	gtc	tcc	tca	ggg	ggg	ggg	ggg	tcc	ggg	ggg	ggg	432
20	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
						130					135					140	
	ggg	tcc	ggg	ggg	ggc	gga	tcc	gat	gtt	gtg	atg	acc	caa	agt	cca	ctc	480
25	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	
	145					150					155					160	
	tcc	ctg	cct	gtc	agt	ctt	gga	gat	caa	gcc	tcc	atc	tct	tgc	aga	tca	528
30	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	
						165					170					175	
	agt	cag	agc	ctt	gtg	cac	agt	aat	gga	aag	acc	tat	tta	cat	tgg	tac	576
35	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Lys	Thr	Tyr	Leu	His	Trp	Tyr	
						180					185					190	
	ctg	cag	aag	cca	ggc	cag	tct	cca	aaa	ctc	ctg	atc	tac	aaa	gtt	tcc	624
40	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	
						195					200					205	
	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	gga	tca	gtg	672
45	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Val	
						210					215					220	
	aca	gat	ttc	aca	ctc	atg	atc	agc	aga	gtg	gag	gct	gag	gat	ctg	gga	720
50	Thr	Asp	Phe	Thr	Leu	Met	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	

225                      230                      235                      240  
 5    gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg ttc gga ggg 768  
     Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly  
                          245                      250                      255  
 10    ggg acc aag ctg gaa ata aaa ggt ggt ggt ggt tcg ggt ggt ggt ggt 816  
     Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly  
                          260                      265                      270  
 15    tcg ggt ggt ggc gga tcg gtc gac tcc cag gtc cag ctg cag cag tct 864  
     Ser Gly Gly Gly Gly Ser Val Asp Ser Gln Val Gln Leu Gln Gln Ser  
 20                      275                      280                      285  
     gga cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc aag 912  
     Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys  
 25                      290                      295                      300  
     gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag cag 960  
     Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln  
 30                      305                      310                      315                      320  
     aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat 1008  
     Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn  
 35                      325                      330                      335  
     gat ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act 1056  
     Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr  
 40                      340                      345                      350  
     tca gac aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc 1104  
     Ser Asp Lys Ser Ser Thr Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala  
 45                      355                      360                      365  
     tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act 1152  
     Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr  
 50                      370                      375                      380  
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5      tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcc tca ggt ggt 1200  
 Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly  
 385                      390                      395                      400  
 10      ggt ggt tcg ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gat gtt gtg 1248  
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val  
                     405                      410                      415  
 15      atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc 1296  
 Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala  
                     420                      425                      430  
 20      tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt aat gga aag 1344  
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys  
                     435                      440                      445  
 25      acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc 1392  
 Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu  
                     450                      455                      460  
 30      ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc 1440  
 Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe  
 465                      470                      475                      480  
 35      agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg 1488  
 Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu Met Ile Ser Arg Val  
                     485                      490                      495  
 40      gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt 1536  
 Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val  
                     500                      505                      510  
 45      ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa 1584  
 Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys  
 50                      515                      520                      525  
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**Asp Asp Asp Asp Lys**

5                   **530**

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35           <223> PCR primer

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45

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<210> 37

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EP 1 327 680 B1

<400> 37  
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EP 1 327 680 B1

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&lt;220&gt;

&lt;221&gt; CDS

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&lt;223&gt; CF2HL-0/pCOS1. MABL2-scFv&lt;HL-0&gt;

&lt;400&gt; 48

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15

5 10 15  
 gac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag cct ggg 102  
 Asp Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly

20

20 25 30  
 gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc gct aac cat 153  
 Ala Ser Val Lys MET Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn His

25

35 40 45 50  
 gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt gag tgg att gga 204  
 Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly

30

55 60 65  
 tat att tat cct tac aat gat ggt act aag tat aat gag aag ttc aag gac 255  
 Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp

35

70 75 80 85  
 aag gcc act ctg act tca gac aaa tcc tcc acc aca gcc tac atg gac ctc 306  
 Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu

40

90 95 100  
 agc agc ctg gcc tct gag gac tct gcg gtc tat tac tgt gca aga ggg ggt 357  
 Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly

45

105 110 115

50

55

5      tac tat act tac gac gac tgg ggc caa ggc acc act ctc aca gtc tcg agt 408  
 Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
 120                      125                      130                      135  
 10      gac gtc gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga gat 459  
 Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp  
 140                      145                      150  
 15      caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt aat gga 510  
 Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly  
 155                      160                      165                      170  
 20      aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca aaa ctc 561  
 Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu  
 175                      180                      185  
 25      ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt 612  
 Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser  
 190                      195                      200  
 30      ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg gag gct 663  
 Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val Glu Ala  
 205                      210                      215                      220  
 35      gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac acg 714  
 Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr Thr  
 225                      230                      235  
 40      ttc gga ggg ggg acc aag ctg gaa ata aaa gac tac aaa gac gat gac gat 765  
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp  
 45      240                      245                      250                      255  
 aaa taa tga gga tcc 780  
 Lys

50

&lt;210&gt; 49

&lt;211&gt; 45

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

# EP 1 327 680 B1

<223> PCR primer

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15

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5

MET Lys Leu Pro Val Arg Leu Leu Val Leu MET Phe Trp Ile Pro Gly Ser -

5

10

15

10

15

20

25

30

35

40

45

50

55

agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt 102  
 5 Ser Ser Asp Val Val MET Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu  
           20                          25                          30  
 gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt gtg cac agt 153  
 10 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser  
           35                          40                          45                          50  
 aat gga aag acc tat tta cat tgg tac ctg cag aag cca ggc cag tct cca 204  
 15 Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro  
                           55                          60                          65  
 aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg 255  
 20 Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg  
           70                          75                          80                          85  
 ttc agt ggc agt gga tca gtg aca gat ttc aca ctc atg atc agc aga gtg 306  
 25 Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr Leu MET Ile Ser Arg Val  
                           90                          95                          100  
 gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg 357  
 30 Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro  
           105                          110                          115  
 tac acg ttc gga ggg ggg acc aag ctc gag ata aaa cag gtc caa ttg cag 408  
 35 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gln Val Gln Leu Gln  
           120                          125                          130                          135  
 cag tct gga cct gaa ctg gta aag cct ggg gct tca gtg aag atg tcc tgc 459  
 40 Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys MET Ser Cys  
                           140                          145                          150  
 aag gct tct gga tac acc ttc gct aac cat gtt att cac tgg gtg aag cag 510  
 45 Lys Ala Ser Gly Tyr Thr Phe Ala Asn His Val Ile His Trp Val Lys Gln  
           155                          160                          165                          170  
 aag cca ggg cag ggc ctt gag tgg att gga tat att tat cct tac aat gat 561  
 55

Lys Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp  
 5 175 180 185  
 ggt act aag tat aat gag aag ttc aag gac aag gcc act ctg act tca gac 612  
 Gly Thr Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr Ser Asp  
 10 190 195 200  
 aaa tcc tcc acc aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac 663  
 Lys Ser Ser Thr Thr Ala Tyr MET Asp Leu Ser Ser Leu Ala Ser Glu Asp  
 15 205 210 215 220  
 tct gcg gtc tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg 714  
 Ser Ala Val Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp  
 20 225 230 235  
 ggc caa ggc acc act ctc aca gtc tcc tca gac tac aaa gac gat gac gat 765  
 Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp Tyr Lys Asp Asp Asp Asp  
 25 240 245 250 255  
 aaa taa tga gga tcc 780

30 Lys

35 <210> 55  
 <211> 351  
 <212> DNA  
 <213> Human

40 <220>  
 <221> CDS  
 <222> (1)... (351)  
 <223> 12B5HV. 1-351 peptide

45 <400> 55

cag gtg cag ctg gtg cag tct ggg gga ggc ttg gtc cgg ccc ggg ggg 48  
 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

50

55



1                      5                      10                      15  
 5    tcc ctg agt ctc tcc tgt gca gtc tct gga atc acc ctc agg acc tac    96  
     Ser Leu Ser Leu Ser Cys Ala Val Ser Gly Ile Thr Leu Arg Thr Tyr  
                     20                      25                      30  
 10    ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg    144  
     Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                     35                      40                      45  
 15    gca ggt ata tcc ttt gac gga aga agt gaa tac tat gca gac tcc gtg    192  
     Ala Gly Ile Ser Phe Asp Gly Arg Ser Glu Tyr Tyr Ala Asp Ser Val  
                     50                      55                      60  
 20    cag ggc cga ttc acc atc tcc aga gac agt tcc aag aac acc ctg tat    240  
     Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser Ser Lys Asn Thr Leu Tyr  
                     65                      70                      75                      80  
 25    ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt    288  
     Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                     85                      90                      95  
 30    gcg aga gga gca cat tat ggt ttc gat atc tgg ggc caa ggg aca atg    336  
     Ala Arg Gly Ala His Tyr Gly Phe Asp Ile Trp Gly Gln Gly Thr Met  
                     100                      105                      110  
 35    gtc acc gtc tcg agt    351  
     Val Thr Val Ser Ser  
 40                      115

45    <210> 56  
     <211> 57  
     <212> DNA  
     <213> Human

50    <220>  
     <221> CDS  
     <222> (1)...(57)  
     <223> reader sequence

55    <400> 56

atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt tta aga ggt 48  
 Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly  
 5 5 10 15  
 gtc cag tgt 57  
 Val Gln Cys  
 10  
 <210> 57  
 <211> 115  
 15 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> 12B5VH-1  
 20 <400> 57  
 atggagtttg ggctgagctg gggttttctc gttgctcttt taagagggtg ccagtgtcag 60  
 25 gtgcagctgg tgcagtctgg gggaggcttg gtccggcccg gggggtcctt gattc 115  
 <210> 58  
 <211> 115  
 <212> DNA  
 <213> Artificial Sequence  
 30 <220>  
 <223> 12B5VH-2  
 <400> 58  
 40 aaggatatac ctgccaccca ctccagcccc ttgcttgag cctggcggac ccagtgcatt 60  
 ccgtaggtcc tgagggtgat tccagagact gcacaggaga gactcaggga ccccc 115  
 45 <210> 59  
 <211> 115  
 <212> DNA  
 50 <213> Artificial Sequence  
 <220>  
 <223> 12B5VH-3  
 55 <400> 59

EP 1 327 680 B1

**ggcaggtata tcctttgacg gaagaagtga atactatgca gactcogtgc agggccgatt 60**  
**caccatctcc agagacagtt ccaagaacac cctgtatctg caaatgaaca gcctg 115**

5

<210> 60  
 <211> 108  
 <212> DNA  
 <213> Artificial Sequence

10

<220>  
 <223> 12BSVH-4

15

<400> 60

**actcgagacg gtgaccattg tcccttggcc ccagatatcg aaaccataat gtgctcctct 60**  
**cgcacagtaa tacacagccg tgcctcggc tctcaggctg ttcatttg 108**

20

<210> 61  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

25

<220>  
 <223> 12B5VH-S, PCR primer

30

<400> 61  
 ttcaagcttc caccatggag ttgggctga gc 32

35

<210> 62  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

40

<220>  
 <223> 12B5VH-A, PCR primer

<400> 62  
 ttgggatcca ctcaccactc gagacggtga ccat 34

45

<210> 63  
 <211> 588  
 <212> DNA  
 <213> Human

50

<220>  
 <221> CDS  
 <222> (236)... (558)  
 <223> 1-235;intron, 236-558;Human IgG constant region (partial)

55

<400> 63

gaattcgtga gtggatccca agctagcttt ctggggcagg ccaggcctga ctttggcttt 60  
 ggggcaggga gggggctaag gtgaggcagg tggcgccagc cagggtgcaca cccaatgccc 120  
 5 atgagcccag acactggacg ctgaacctcg cggacagtta agaaccagg ggcctctgcg 180  
 ccctgggccc agctctgtcc cacaccgagg tcacatggca caacctctct tgca gcc 237  
 Ala  
 10 1  
 15  
 tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc 285  
 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser  
 20 5 10 15  
 acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc 333  
 Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe  
 25 20 25 30  
 ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc 381  
 Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly  
 30 35 40 45  
 gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc 429  
 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu  
 35 50 55 60 65  
 agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac 477  
 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr  
 40 70 75 80  
 atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa 525  
 Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys  
 45 85 90 95  
 gtt gag ccc aaa tct tgt gac aaa act cac aca 558  
 50 Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
 100 105  
 55

<210> 64  
 <211> 27  
 <212> DNA

# EP 1 327 680 B1

<213> Artificial Sequence

<220>

<223> G1CH1-S, PCR primer

5

<400> 64

tgagaattcg tgagtggatc ccaagct 27

<210> 65

10

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

15

<223> G1CH1-A, PCR primer

<400> 65

aaaagatctt tatcatgtgt gagtttgtc acaagatttg ggctcaactt tctgtccac 60

20

<210> 66

<211> 432

<212> DNA

<213> Human

25

<220>

<221> CDS

<222> (12)... (419)

<223> HEF-12B5H-g gamma. 12-419 peptide

30

<400> 66

aagcttccac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt 50

35

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu

1

5

10

tta aga ggt gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc 98

40

Leu Arg Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly

15

20

25

ttg gtc cgg ccc ggg ggg tcc ctg agt ctc tcc tgt gca gtc tct gga 146

45

50

55

5      Leu Val Arg Pro Gly Gly Ser Leu Ser Leu Ser Cys Ala Val Ser Gly  
       30                      35                      40                      45  
 atc acc ctc agg acc tac ggc atg cac tgg gtc cgc cag gct cca ggc 194  
 Ile Thr Leu Arg Thr Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly  
 10                      50                      55                      60  
 aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga agt gaa 242  
 Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg Ser Glu  
 15                      65                      70                      75  
 tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt 290  
 Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser  
 20                      80                      85                      90  
 tcc aag aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac 338  
 Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
 25                      95                      100                      105  
 acg gct gtg tat tac tgt gcg aga gga gca cat tat ggt ttc gat atc 386  
 Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ala His Tyr Gly Phe Asp Ile  
 30                      110                      115                      120                      125  
 tgg ggc caa ggg aca atg gtc acc gtc tgc agt ggtgagtgga tcc 432  
 Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
                     130                      135

40

&lt;210&gt; 67

&lt;211&gt; 321

&lt;212&gt; DNA

45

&lt;213&gt; Human

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (321)

50

&lt;223&gt; 12B5LV. 1-321 peptide

&lt;400&gt; 67

55

5           gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct att gga 48  
           Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly  
           1                           5                           10                           15  
 10           gac aga gtc acc atc acc tgc cgg gcc agc gag ggt att tat cac tgg 96  
           Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr His Trp  
                   20                           25                           30  
 15           ttg gcc tgg tat cag cag aag cca ggg aaa gcc cct aaa ctc ctg atc 144  
           Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   35                           40                           45  
 20           tat aag gcc tct agt tta gcc agt ggg gcc cca tca agg ttc agc ggc 192  
           Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly  
                   50                           55                           60  
 25           agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct 240  
           Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
                   65                           70                           75                           80  
 30           gat gat ttt gca act tat tac tgc caa caa tat agt aat tat ccg ctc 288  
           Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu  
                           85                           90                           95  
 35           act ttc ggc gga ggg acc aag ctg gag atc aaa 321  
           Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
                   100                           105

40           <210> 68  
           <211> 66  
           <212> DNA  
           <213> Human

45           <220>  
           <221> CDS  
           <222> (1)... (66)  
           <223> reader sequence

50           <400> 68

EP 1 327 680 B1

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48

MET Asp MET Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp

5 5 10 15

ctc cca ggt gcc aaa tgt 66

Leu Pro Gly Ala Lys Cys

10 20

15 <210> 69  
<211> 110  
<212> DNA  
<213> Artificial Sequence

20 <220>  
<223> 12B5VL-1

<400> 69

25 atggacatga ggggtccccgc tcagctcctg gggtcctgc tgctctgget cccaggtgcc 60

aaatgtgaca tccagatgac ccagtctcct tccaccctgt ctgcatctat 110

30 <210> 70  
<211> 110  
<212> DNA  
35 <213> Artificial Sequence

<220>  
<223> 12B5VL-2

40 <400> 70

ggagtttagg ggctttccct ggctttctgt gataccagge caaccagtga taaataccct 60

45 cgctggcccg gcaggtgatg gtgactctgt ctccaataga tgcagacagg 110

50 <210> 71  
<211> 110  
<212> DNA  
<213> Artificial Sequence

55 <220>  
<223> 12B5VL-3

<400> 71



EP 1 327 680 B1

**aagcccctaa actcctgata tataaggcct ctagtttagc cagtggggcc ccatcaaggt 60**  
**tcagcggcag tggatctggg acagatttca ctctaccat cagcagcctg 110**

5

<210> 72  
 <211> 103  
 <212> DNA  
 <213> Artificial Sequence

10

<220>  
 <223> 12B5VL-4

15

<400> 72

**tttgatctcc agcttgggtcc ctccgccgaa agtgagcgga taattactat attgttgga 60**  
**gtaataagtt gcaaaatcat caggctgcag gctgctgatg gtg 103**

20

<210> 73  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

25

<220>  
 <223> 12B5VL-S; PCR primer

30

<400> 73  
 ttcaagcttc caccatggac atgagggtcc cc 32

<210> 74  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

35

<220>  
 <223> 12B5VL-A, PCR primer

40

<400> 74  
 tctaggatcc actcacgttt gatctccagc ttggt 35

<210> 75  
 <211> 415  
 <212> DNA  
 <213> Human

45

<220>  
 <221> CDS  
 <222> (12)... (398)  
 <223> HEF-12B5H-g kappa. 12-398 peptide

50

<400> 75

55

aagcttccac c atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg 50  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu  
 5 1 5 10  
 ctg ctc tgg ctc cca ggt gcc aaa tgt gac atc cag atg acc cag tct 98  
 Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser  
 10  
 15 15 20 25  
 cct tcc acc ctg tct gca tct att gga gac aga gtc acc atc acc tgc 146  
 Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys  
 20 30 35 40 45  
 cgg gcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag aag 194  
 Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln Lys  
 25 50 55 60  
 cca ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt tta gcc 242  
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala  
 30 65 70 75  
 agt ggg gcc cca tca agg ttc agc ggc agt gga tct ggg aca gat ttc 290  
 Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
 35 80 85 90  
 act ctc acc atc agc agc ctg cag cct gat gat ttt gca act tat tac 338  
 Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr  
 40 95 100 105  
 tgc caa caa tat agt aat tat ccg ctc act ttc ggc gga ggg acc aag 386  
 Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys  
 45 110 115 120 125  
 ctg gag atc aaa cgtgagtggg tctaga 415  
 50 Leu Glu Ile Lys

55 <210> 76  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> FLAG tag sequence

<400> 76

5

**gac tac aag gat gac gac gat aag 24**

**Asp Tyr Lys Asp Asp Asp Lys**

10

**5**

<210> 77

<211> 31

15

<212> DNA

<213> Artificial Sequence

<220>

<223> 12B5-S, PCR primer

20

<400> 77

atagaattcc accatggagt ttggctgag c 31

<210> 78

25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

30

<223> HuVHJ3, PCR primer

<400> 78

tgaagagacg gtgaccattg tccc 24

<210> 79

35

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

40

<223> RhuJH3, PCR primer

<400> 79

ggacaatggt caccgtctct tcaggtgg 28

45

<210> 80

<211> 32

<212> DNA

<213> Artificial Sequence

50

<220>

<223> RhuVK1, PCR primer

<400> 80

55

ggagactggg tcattctgat gtccgatccg cc 32

<210> 81

<211> 23

EP 1 327 680 B1

<212> DNA  
<213> Artificial Sequence

5 <220>  
<223> HuVK1.2, PCR primer

<400> 81  
gacatccaga tgacccagtc tcc 23

10 <210> 82  
<211> 59  
<212> DNA  
<213> Artificial Sequence

15 <220>  
<223> 12B5F-A, PCR primer

20 <400> 82  
attgcggccg cttatcactt atcgtcgtca tcctttagt cttgatctc cagcttgg 59

<210> 83  
<211> 45  
<212> DNA  
<213> Artificial Sequence

25 <220>  
<223> Linker amino acid sequence and nucleotide sequence

30 <400> 83

**ggt ggt ggt ggt tgc ggt ggt ggt ggt tgc ggt ggt ggc gga tgc 45**  
**Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser**

35 5 10 15

40 <210> 84  
<211> 823  
<212> DNA  
<213> Human

45 <220>  
<221> CDS  
<222> (12)...(809)  
<223> sc12B5, Single chain Fv

50 <400> 84

55

aagcttcac c atg gag ttt ggg ctg agc tgg gtt ttc ctc gtt gct ctt 50

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu

5

1

5

10

tta aga ggt gtc cag tgt cag gtg cag ctg gtg cag tct ggg gga ggc 98

Leu Arg Gly Val Gln Cys Gln Val Gln Leu Val Gln Ser Gly Gly Gly

10

15

20

25

30

35

40

45

50

55

	15	20	25	
5	ttg gtc cgg ccc ggg ggg tcc ctg agt ctc tcc tgt gca gtc tct gga	146		
	Leu Val Arg Pro Gly Gly Ser Leu Ser Leu Ser Cys Ala Val Ser Gly			
	30	35	40	45
10	atc acc ctc agg acc tac ggc atg cac tgg gtc cgc cag gct cca ggc	194		
	Ile Thr Leu Arg Thr Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly			
	50	55	60	
15	aag ggg ctg gag tgg gtg gca ggt ata tcc ttt gac gga aga agt gaa	242		
	Lys Gly Leu Glu Trp Val Ala Gly Ile Ser Phe Asp Gly Arg Ser Glu			
	65	70	75	
20	tac tat gca gac tcc gtg cag ggc cga ttc acc atc tcc aga gac agt	290		
	Tyr Tyr Ala Asp Ser Val Gln Gly Arg Phe Thr Ile Ser Arg Asp Ser			
	80	85	90	
25	tcc aag aac acc ctg tat ctg caa atg aac agc ctg aga gcc gag gac	338		
	Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp			
	95	100	105	
30	acg gct gtg tat tac tgt gcg aga gga gca cat tat ggt ttc gat atc	386		
	Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ala His Tyr Gly Phe Asp Ile			
	110	115	120	125
35	tgg ggc caa ggg aca atg gtc acc gtc tcg agt ggt ggt ggt ggt tcg	434		
	Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser			
	130	135	140	
40	ggt ggt ggt ggt tcg ggt ggt ggc gga tcg gac atc cag atg acc cag	482		
	Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln			
	145	150	155	
45	tct cct tcc acc ctg tct gca tct att gga gac aga gtc acc atc acc	530		
	Ser Pro Ser Thr Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr			
	160	165	170	
50				
55				

tgc cgg gcc agc gag ggt att tat cac tgg ttg gcc tgg tat cag cag 578

Cys Arg Ala Ser Glu Gly Ile Tyr His Trp Leu Ala Trp Tyr Gln Gln

175

180

185

aag cca ggg aaa gcc cct aaa ctc ctg atc tat aag gcc tct agt tta 626

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Ser Leu

190

195

200

205

gcc agt ggg gcc cca tca agg ttc agc ggc agt gga tct ggg aca gat 674

Ala Ser Gly Ala Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

210

215

220

ttc act ctc acc atc agc agc ctg cag cct gat gat ttt gca act tat 722

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr

225

230

235

TAC TGC CAA CAA TAT AGT AAT TAT CCG CTC ACT TTC GGC GGA GGG ACC 770

Tyr Cys Gln Gln Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr

240

245

250

aag ctg gag atc aaa gac tac aag gat gac gac gat aag tgataagcgg c 820

Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys

255

260

265

cgc

823

<210> 85

<211> 114

<212> PRT

<213> Human

<400> 85

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Glu

1

5

10

15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Tyr  
 5                    20                    25                    30  
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
                   35                    40                    45  
 10 Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys  
                   50                    55                    60  
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Ser Gln Phe Ser Leu  
 15                    65                    70                    75                    80  
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
                   85                    90                    95  
 20 Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg Gly Thr Met Val Thr Val  
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 25 Ser Ser

<210> 86

<211> 342

<212> DNA

<213> Human

<400> 86

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 40 ccaggaagg gactggagtg gattgggtat atctattaca gtgggagcac caactacaac 180  
 ccctccctca agagtcgagt caccatatca gtagacaagt ecaagagcca gttctccctg 240  
 aagctgagct ctgtgaccgc cgcagacacg gccgtgtatt actgtgcgag agggcggtag 300  
 45 ttcgatgtct ggggccgtgg caccatggtc actgtctcct ca 342

<210> 87

<211> 57

<212> DNA

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<220>

<221> CDS

<222> (1)... (57)

<223> reader sequence



**EP 1 327 680 B1**

<308> GenBank No. AF062252

<400> 87

[illegible]

15 .

<210> 88

<211> 110

<212> DNA

20 <213> Artificial Sequence

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gtgcagctgc agcagtcggg cccaggactg gtgaagcctt cggagaccct 110

35

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<211>	110
<212>	DNA
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<220>  
<223> 12E10VH2

<400> 89

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         tgatggagtc accagagaca gtgcagggtga gggacagggt ctccgaaggc      110

50

<210> 90  
<211> 110  
<212> DNA  
<213> Artificial Sequence

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         <223> 12E10VH3

<400> 90

EP 1 327 680 B1

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              **gtcaggtcac catatcagta gacacgtcca agagccagtt ctccctgaag                110**

10            <210> 91  
              <211> 114  
              <212> DNA  
              <213> Artificial Sequence

             <220>  
              <223> 12E10VH4

15            <400> 91

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 20            **gtaatacacg gccgtgtctg cggcgggtcac agagctcagc ttcagggaga actg                114**

25            <210> 92  
              <211> 32  
              <212> DNA  
              <213> Artificial Sequence

30            <220>  
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             <400> 92  
              ttcaagcttc caccatgaaa catctgtggt tc                32

35            <210> 93  
              <211> 34  
              <212> DNA  
              <213> Artificial Sequence

40            <220>  
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             <400> 93  
              ttgggatcca ctacctgag gagacagtga ccat                34

45            <210> 94  
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              <212> DNA  
              <213> Mus

50            <220>  
              <221> CDS  
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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala

5

10

1 5 10

ccc aga tgg gtc ctg tcc cag gtg cag ctg cag cag tgc ggc cca gga 98

Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Gly

15

15 20 25

ctg gtg aag cct tgc gag acc ctg tcc ctc acc tgc act gtc tct ggt 146

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly

20

30 35 40 45

gac tcc atc agt agt tac tac tgg agc tgg att cgg cag ccc cca ggg 194

Asp Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly

25

50 55 60

aag gga ctg gag tgg att ggg tat atc tat tac agt ggg agc acc aac 242

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn

30

65 70 75

tac aac ccc tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc 290

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser

35

80 85 90

aag agc cag ttc tcc ctg aag ctg agc tct gtg acc gcc gca gac acg 338

Lys Ser Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr

40

95 100 105

gcc gtg tat tac tgt gcg aga ggg cgg tac ttc gat gtc tgg ggc cgt 386

Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg

45

110 115 120 125

ggc acc atg gtc act gtc tcc tca ggtgagtga tcccaa 426

Gly Thr Met Val Thr Val Ser Ser

50

130

55

<210> 95  
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<212> PRT

EP 1 327 680 B1

<213> Mus

<400> 95

5

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ser Pro Gly Gln

1 5 10 15

10

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr

20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu

15

35 40 45

Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe

50 55 60

20

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu

65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Thr Arg

25

85 90 95

Ser Thr Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

30

100 105 110

<210> 96

<211> 330

35

<212> DNA

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<400> 96

40

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tcctgcactg gaaccagcag tgacgttggt ggttataact atgtctcctg gtaccaacag 120

45

caccagggca aagcccccaa actcatgatt tatgagggca gtaaaccggcc ctcaggggtt 180

50

tctaategct tctctggctc caagtctggc aacacggcct ccctgaccat ctctgggctc 240

caggctgagg acgaggctga ttattactgc agctcatata caaccagaag cactcgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

55

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<211> 57

EP 1 327 680 B1

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<222> (1)... (57)  
<223> reader sequence

<310>

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Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly

1 5 10 15

tct gtg acc 57

Ser Val Thr

<210> 98  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> 12E10VL1, PCR primer

<400> 98

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tatgtgctga ctcagccacc ctcgggtgtca gggctctcctg gacagtcgat 110

<210> 99  
<211> 62  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 12E10VL2, PCR primer

<400> 99

tcatgagttt gggggctttg cctgggtgct gttggtacca ggagacatag ttataaccac 60

caacgtcact gctggttcca gtgcaggaga tggatgatcga ctgtccagga 110

# EP 1 327 680 B1

<210> 100  
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 <213> Artificial Sequence

5

<220>  
 <223> 12E10VL3, PCR primer

<400> 100

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**cccccaaact catgatttat gagggcagta aacggccctc aggggtttct aatcgttct 60**  
**ctggctccaa gtctggcaac acggcctccc tgaccatctc tgggctccag 110**

15

<210> 101  
 <211> 102  
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<220>  
 <223> 12E10VL4, PCR primer

25

<400> 101

**taggacggtc agcttgggcc ctcgccgaa caccgagtg cttctggttg tatatgagct 60**  
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<210> 102  
 <211> 31  
 <212> DNA  
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35

<220>  
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40

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45

<220>  
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50

<400> 103  
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<210> 104  
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&lt;221&gt; CDS

&lt;222&gt; (1)... (387)

&lt;223&gt; 12E10L, L chain V region

5

&lt;310&gt;

&lt;400&gt; 104

10

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Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly

1 5 10 15

15

tct gtg acc tcc tat gtg ctg act cag cca ccc tcg gtg tca ggg tct 96

Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ser

20

20 25 30

cct gga cag tcg atc acc atc tcc tgc act gga acc agc agt gac gtt 144

Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val

25

35 40 45

ggg ggt tat aac tat gtc tcc tgg tac caa cag cac cca ggc aaa gcc 192

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala

30

50 55 60

ccc aaa ctc atg att tat gag ggc agt aaa cgg ccc tca ggg gtt tct 240

Pro Lys Leu Met Ile Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser

35

65 70 75 80

aat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc 288

Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile

40

85 90 95

tct ggg ctc cag gct gag gac gag gct gat tat tac tgc agc tca tat 336

Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr

45

100 105 110

Aca acc aga agc act cgg gtg ttc ggc gga ggg acc aag ctg acc gtc 384

Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val

50

115 120 125

55

**cta****387****Leu**

5

<210> 105  
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 <222> (1)... (24)  
 <223> FLAG, reader sequence

15

&lt;400&gt; 105

20

**gac tac aag gat gac gac gat aag      24**  
**Asp Tyr Lys Asp Asp Asp Asp Lys**

25

<210> 106  
 <211> 30  
 <212> DNA  
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 <223> 12E10S, PCR primer

<400> 106  
 tatgaattcc accatgaaac atctgtggtt      30

35

<210> 107  
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40

<220>  
 <223> DB2, PCR primer

<400> 107  
 taggagctac cgctccacc tgaggagaca gtgacat      38

45

<210> 108  
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 <212> DNA  
 <213> Artificial Sequence

50

<220>  
 <223> DB1, PCR primer

<400> 108  
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55



EP 1 327 680 B1

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<220>  
<223> 12E10FA, PCR primer

<400> 109  
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10

59

<210> 110  
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15

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<223> 12E10, Single chain Fv

20

<400> 110

25

30

35

40

45

50

55

gaattccacc atg aaa cat ctg tgg ttc ttc ctt ctc ctg gtg gca gct 49

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala

5

1

5

10

ccc aga tgg gtc ctg tcc cag gtg cag ctg cag cag tcg ggc cca gga 97

Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Gly

10

15

20

25

ctg gtg aag cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt 145

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly

15

30

35

40

45

gac tcc atc agt agt tac tac tgg agc tgg att cgg cag ccc cca ggg 193

Asp Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly

20

50

55

60

aag gga ctg gag tgg att ggg tat atc tat tac agt ggg agc acc aac 241

Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn

25

65

70

75

tac aac ccc tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc 289

Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser

30

80

85

90

aag agc cag ttc tcc ctg aag ctg agc tct gtg acc gcc gca gac acg 337

Lys Ser Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr

35

95

100

105

gcc gtg tat tac tgt gcg aga ggg cgg tac ttc gat gtc tgg ggc cgt 385

Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg

40

110

115

120

125

45

50

55

5      ggc acc atg gtc act gtc tcc tca ggt gga ggc ggt agc tcc tat gtg 433  
      Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Ser Tyr Val  
                  130                              135                              140  
 10      ctg act cag cca ccc tgc gtg tca ggg tct cct gga cag tgc atc acc 481  
      Leu Thr Gln Pro Pro Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr  
                  145                              150                              155  
 15      atc tcc tgc act gga acc agc agt gac gtt ggt ggt tat aac tat gtc 529  
      Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val  
                  160                              165                              170  
 20      tec tgg tac caa cag cac cca ggc aaa gcc ccc aaa ctc atg att tat 577  
      Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr  
                  175                              180                              185  
 25      gag ggc agt aaa cgg ccc tca ggg gtt tct aat cgc ttc tct ggc tcc 625  
      Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser  
      190                              195                              200                              205  
 30      aag tct ggc aac acg gcc tcc ctg acc atc tct ggg ctc cag gct gag 673  
      Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu  
                  210                              215                              220  
 35      gac gag gct gat tat tac tgc agc tca tat aca acc aga agc act cgg 721  
      Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Thr Arg Ser Thr Arg  
                  225                              230                              235  
 40      gtg ttc ggc gga ggg acc aag ctg acc gtc cta gac tac aag gat gac 769  
      Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Asp Tyr Lys Asp Asp  
                  240                              245                              250  
 45      gac gat aag tgataagcgg ccgc 792  
      Asp Asp Lys  
 50      255  
 55      <210> 111  
      <211> 62  
      <212> DNA

EP 1 327 680 B1

<213> Artificial Sequence

<220>

<223> sc4.3, PCR primer

5

<400> 111

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10

**cc 62**

<210> 112

15

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

20

<223> sc1.3, PCR primer

<400> 112

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25

**g 61**

<210> 113

30

<211> 822

<212> DNA

<213> Artificial Sequence

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<220>

<221> CDS

<222> (11) ... (807)

<223> sc12E10, Single chain Fv

40

<400> 113

45

50

55

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 5                   1                   5                   10  
 ccc aga tgg gtc ctg tcc cag gtg cag ctg cag cag tcg ggc cca gga 97  
 Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Gly  
 10                   15                   20                   25  
 ctg gtg aag cct tcg gag acc ctg tcc ctc acc tgc act gtc tct ggt 145  
 Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly  
 15                   30                   35                   40                   45  
 gac tcc atc agt agt tac tac tgg agc tgg att cgg cag ccc cca ggg 193  
 Asp Ser Ile Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly  
 20                   50                   55                   60  
 aag gga ctg gag tgg att ggg tat atc tat tac agt ggg agc acc aac 241  
 Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn  
 25                   65                   70                   75  
 tac aac ccc tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc 289  
 Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser  
 30                   80                   85                   90  
 aag agc cag ttc tcc ctg aag ctg agc tct gtg acc gcc gca gac acg 337  
 Lys Ser Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr  
 35                   95                   100                   105  
 gcc gtg tat tac tgt gcg aga ggg cgg tac ttc gat gtc tgg ggc cgt 385  
 Ala Val Tyr Tyr Cys Ala Arg Gly Arg Tyr Phe Asp Val Trp Gly Arg  
 40                   110                   115                   120                   125  
 ggc acc atg gtc act gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt 433  
 Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 45                   130                   135                   140  
 50  
 55

	ggc tgc ggt ggt ggc gga tgc tcc tat gtg ctg act cag cca ccc tgc	481
5	Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser	
	145 150 155	
	gtg tca ggg tct cct gga cag tgc atc acc atc tcc tgc act gga acc	529
10	Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile Ser Cys Thr Gly Thr	
	160 165 170	
	agc agt gac gtt ggt ggt tat aac tat gtc tcc tgg tac caa cag cac	577
15	Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln His	
	175 180 185	
	cCa ggc aaa gcc ccc aaa ctc atg att tat gag ggc agt aaa cgg ccc	625
20	Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Glu Gly Ser Lys Arg Pro	
	190 195 200 205	
	tca ggg gtt tct aat cgc ttc tct ggc tcc aag tct ggc aac acg gcc	673
25	Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala	
	210 215 220	
	tcc ctg acc atc tct ggg etc cag gct gag gac gag gct gat tat tac	721
30	Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr	
	225 230 235	
	tgc agc tca tat aca acc aga agc act cgg gtg ttc ggc gga ggg acc	769
35	Cys Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr	
	240 245 250	
	aag ctg acc gtc cta gac tac aag gat gac gac gat aag tgataagcgg	818
40	Lys Leu Thr Val Leu Asp Tyr Lys Asp Asp Asp Asp Lys	
	255 260 265	
45	ccgc	822

## Claims

1. A modified antibody comprising two or more H chain V regions and two or more L chain V regions of an antibody and showing TPO agonist action by crosslinking TPO receptor, wherein the modified antibody is:
- (i) a multimer of single chain Fv comprising an H chain V region and an L chain V region; or
  - (ii) a single chain polypeptide comprising two or more H chain V regions and two or more L chain V regions.

2. The modified antibody of claim 1, wherein the H chain V region and the L chain V region are connected through a linker.
3. The modified antibody of claim 2 or 3, wherein the linker is a peptide linker comprising at least one amino acid.
- 5 4. The modified antibody of any one of claims 1 to 3, wherein the modified antibody is composed of tetramer, trimer or dimer of single chain Fv.
5. The modified antibody of claim 4, wherein the modified antibody is composed of dimer of single chain Fv.
- 10 6. The modified antibody of any one of claims 1 to 3, wherein the modified antibody is a single chain polypeptide comprising two H chain V regions and two L chain V regions.
7. The modified antibody of any one of claims 1 to 6, wherein the modified antibody further comprises an amino acid sequence(s) for peptide purification.
- 15 8. The modified antibody of any one of claims 1 to 7, wherein the modified antibody has been purified.
9. The modified antibody of any one of claims 1 to 8, wherein H chain V region and/or L chain V region is H chain V region and/or L chain V region derived from a human antibody.
- 20 10. The modified antibody of any one of claims 1 to 9, wherein H chain V region and/or L chain V region is humanised H chain V region and/or L chain V region.
11. The modified antibody of any one of claims 1 to 10, wherein modified antibody is mono-specific modified antibody.
- 25 12. The modified antibody of any one of claims 1 to 10, wherein the modified antibody is multi-specific modified antibody.
13. The modified antibody of claim 12, wherein the modified antibody is bi-specific modified antibody.
- 30 14. The modified antibody of claim 11, wherein the L chain V region and the H chain V region are from the same monoclonal antibody.
15. The modified antibody of any one of claims 1 to 14, which is derived from a parent antibody having substantially no agonist action.
- 35 16. A DNA which encodes the modified antibody of any one of claims 1 to 15.
17. An animal cell which produces the modified antibody of any one of claims 1 to 15.
- 40 18. A microorganism which produces the modified antibody of any one of claims 1 to 15.
19. A medicine comprising as active ingredient the modified antibody of any one of claims 1 to 15.
20. Use of the modified antibody of any one of claims 1 to 15 for the preparation of a medicine to treat thrombocytopenia.
- 45 21. A method of screening a modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and showing an agonist action by crosslinking TPO receptor, wherein the modified antibody is
  - (i) a multimer of single chain Fv comprising an H chain V region and an L chain V region; or
  - (ii) a single chain polypeptide comprising two or more H chain V regions and two or more L chain V regions, which comprises the steps
    - (1) to produce a modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and binding specifically to TPO receptor,
    - 55 (2) to subject cells expressing said TPO receptor to react with the modified antibody and
    - (3) to measure TPO agonist action in the cells caused by crosslinking TPO receptor.
22. A method of measuring an agonist action of a modified antibody comprising two or more H chain V regions and two

or more L chain V regions of antibody and showing an agonist action by crosslinking TPO receptor, wherein the modified antibody is

- (i) a multimer of single chain Fv comprising an H chain V region and an L chain V region; or
- (ii) a single chain polypeptide comprising two or more H chain V regions and two or more L chain V regions, which comprises the steps

- (1) to produce a modified antibody comprising two or more H chain V regions and two or more L chain V regions of antibody and binding specifically to TPO receptor,
- (2) to subject cells expressing said TPO receptor to react with the modified antibody and
- (3) to measure TPO agonist action in the cells caused by crosslinking TPO receptor.

23. The modified antibody of any one of claims.1 to 15 for use in a method of treating thrombocytopenia.

#### Patentansprüche

1. Modifizierter Antikörper, welcher TPO-Agonistenaktivität durch Quervernetzen von TPO-Rezeptoren zeigt, umfassend zwei oder mehr H-Ketten V-Regionen und zwei oder mehr L-Ketten V-Regionen eines Antikörpers, worin der modifizierte Antikörper

- (i) ein Multimer eines single chain Fv umfassend eine H-Ketten V-Region und eine L-Ketten V-Region oder
- (ii) ein einzelkettiges Polypeptid umfassend zwei oder mehr H-Ketten V-Regionen oder zwei oder mehr L-Ketten V-Regionen

ist.

2. Modifizierter Antikörper gemäß Anspruch 1, worin die H-Ketten V-Region und die L-Ketten V-Region durch einen Linker verbunden sind.

3. Modifizierter Antikörper gemäß Anspruch 2 oder 3, worin der Linker ein Peptidlinker, umfassend zumindest eine Aminosäure, ist.

4. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 3, worin der modifizierte Antikörper zusammengesetzt ist aus einem Tetramer, Trimer oder Dimer aus single chain Fv.

5. Modifizierter Antikörper gemäß Anspruch 4, worin der modifizierte Antikörper zusammengesetzt ist aus einem Dimer aus single chain Fv.

6. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 3, worin der modifizierte Antikörper ein einzelkettiges Polypeptid umfassend zwei H-Ketten V-Regionen und zwei L-Ketten V-Regionen ist.

7. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 6, worin der modifizierte Antikörper des weiteren Aminosäuresequenz(en) zur Peptidreinigung enthält.

8. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 7, worin der modifizierte Antikörper aufgereinigt wurde.

9. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 8, worin die H-Ketten V-Region und/oder L-Ketten V-Region eine H-Ketten V-Region und/oder L-Ketten V-Region abgeleitet von einem menschlichen Antikörper ist.

10. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 9, worin die H-Ketten V-Region und/oder L-Ketten V-Region eine humanisierte H-Ketten V-Region und/oder L-Ketten V-Region ist.

11. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 10, worin der modifizierte Antikörper ein monospezifischer modifizierter Antikörper ist.

12. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 10, worin der modifizierte Antikörper ein multispezifischer modifizierter Antikörper ist.



13. Modifizierter Antikörper gemäß Anspruch 12, worin der modifizierte Antikörper ein bispezifischer modifizierter Antikörper ist.
14. Modifizierter Antikörper gemäß Anspruch 11, worin die L-Ketten V-Region und die H-Ketten V-Region von demselben monoklonalen Antikörper sind.
15. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 14, welcher abgeleitet ist von einem Stammantikörper, der im wesentlichen keine agonistische Aktivität aufweist.
16. DNA, die den modifizierten Antikörper gemäß einem der Ansprüche 1 bis 15 codiert.
17. Tierische Zelle, welche den modifizierten Antikörper gemäß einem der Ansprüche 1 bis 15 produziert.
18. Mikroorganismus, welcher den modifizierten Antikörper gemäß einem der Ansprüche 1 bis 15 produziert.
19. Medikament, umfassend den modifizierten Antikörper gemäß einem der Ansprüche 1 bis 15 als aktiven Inhaltsstoff.
20. Verwendung des modifizierten Antikörpers gemäß einem der Ansprüche 1 bis 15 zur Herstellung eines Medikaments zur Behandlung von Thrombocytopenie.
21. Verfahren zum Screenen eines modifizierten Antikörpers, welcher agonistische Aktivität durch Quervernetzen des TPO-Rezeptors zeigt, umfassend zwei oder mehr H-Ketten V-Regionen und zwei oder mehr L-Ketten V-Regionen eines Antikörpers, worin der modifizierte Antikörper
  - (i) ein Multimer eines single chain Fv umfassend eine H-Ketten V-Region und eine L-Ketten V-Region oder
  - (ii) ein einzelkettiges Polypeptid umfassend zwei oder mehr H-Ketten V-Regionen oder zwei oder mehr L-Ketten V-Regionenist, umfassend die Schritte
  - (1) Herstellen eines modifizierten Antikörpers, welcher spezifisch an TPO-Rezeptoren bindet, umfassend zwei oder mehr H-Ketten V-Regionen und zwei oder mehr L-Ketten V-Regionen eines Antikörpers,
  - (2) Reagierenlassen der modifizierten Antikörper und Zellen, die besagten TPO-Rezeptor exprimieren, und
  - (3) Messen der TPO-Agonistenaktivität in den Zellen, verursacht durch Quervernetzen des TPO-Rezeptors.
22. Verfahren zur Messung der agonistischen Aktivität eines modifizierten Antikörpers, welcher agonistische Aktivität durch Quervernetzen des TPO-Rezeptors zeigt, umfassend zwei oder mehr H-Ketten V-Regionen und zwei oder mehr L-Ketten V-Regionen eines Antikörpers, worin der modifizierte Antikörper
  - (i) ein Multimer eines single chain Fv umfassend eine H-Ketten V-Region und eine L-Ketten V-Region oder
  - (ii) ein einzelkettiges Polypeptid umfassend zwei oder mehr H-Ketten V-Regionen oder zwei oder mehr L-Ketten V-Regionenist, umfassend die Schritte
  - (1) Herstellen eines modifizierten Antikörpers, welcher spezifisch an TPO-Rezeptoren bindet, umfassend zwei oder mehr H-Ketten V-Regionen und zwei oder mehr L-Ketten V-Regionen eines Antikörpers,
  - (2) Reagierenlassen der modifizierten Antikörper und Zellen, die besagten TPO-Rezeptor exprimieren, und
  - (3) Messen der TPO-Agonistenaktivität in den Zellen, verursacht durch Quervernetzen des TPO-Rezeptors.
23. Modifizierter Antikörper gemäß einem der Ansprüche 1 bis 15 zur Verwendung in einem Verfahren zur Behandlung von Thrombocytopenie.

## Revendications

1. Anticorps modifié comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L d'un anticorps et montrant une action agoniste TPO par réticulation d'un récepteur TPO, où

l'anticorps modifié est:

- (i) un multimère de simple chaîne Fv comprenant une région V d'une chaîne H et une région V d'une chaîne L; ou
- (ii) un polypeptide à simple chaîne comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L.

2. Anticorps modifié de la revendication 1, dans lequel la région V d'une chaîne H et la région V d'une chaîne L sont connectées à travers un lieu.

3. Anticorps modifié de la revendication 2 ou 3, dans lequel le lieu est un lieu peptidique comprenant au moins un acide aminé.

4. Anticorps modifié de l'une quelconque des revendications 1 à 3, dans lequel l'anticorps modifié est composé de tétramère, trimère ou dimère d'une simple chaîne Fv.

5. Anticorps modifié de la revendication 4, dans lequel l'anticorps modifié est composé de dimère d'une simple chaîne Fv.

6. Anticorps modifié de l'une quelconque des revendications 1 à 3, dans lequel l'anticorps modifié est un polypeptide à simple chaîne comprenant deux régions V d'une chaîne H et deux régions V d'une chaîne L.

7. Anticorps modifié de l'une quelconque des revendications 1 à 6, dans lequel l'anticorps modifié comprend en plus une séquence (s) d'acides aminés pour une purification peptidique.

8. Anticorps modifié de l'une quelconque des revendications 1 à 7, dans lequel l'anticorps modifié a été purifié.

9. Anticorps modifié de l'une quelconque des revendications 1 à 8, dans lequel une région V d'une chaîne H et/ou une région V d'une chaîne L est une région V d'une chaîne H et/ou une région V d'une chaîne L dérivée d'un anticorps humain.

10. Anticorps modifié de l'une quelconque des revendications 1 à 9, dans lequel une région V d'une chaîne H et/ou une région V d'une chaîne L est une région V d'une chaîne H et/ou une région V d'une chaîne L humanisée.

11. Anticorps modifié de l'une quelconque des revendications 1 à 10, dans lequel l'anticorps modifié est un anticorps modifié monospécifique.

12. Anticorps modifié de l'une quelconque des revendications 1 à 10, dans lequel l'anticorps modifié est un anticorps modifié multispécifique.

13. Anticorps modifié selon la revendication 12, dans lequel l'anticorps modifié est un anticorps modifié bispécifique.

14. Anticorps modifié selon la revendication 11, dans lequel la région V d'une chaîne L et la région V d'une chaîne H proviennent du même anticorps monoclonal.

15. Anticorps modifié de l'une quelconque des revendications 1 à 14, qui est dérivé à partir d'un anticorps parent n'ayant substantiellement aucune action agoniste.

16. ADN qui code pour l'anticorps modifié de l'une quelconque des revendications 1 à 15.

17. Cellule animale qui produit l'anticorps modifié de l'une quelconque des revendications 1 à 15.

18. Microorganisme qui produit l'anticorps modifié de l'une quelconque des revendications 1 à 15.

19. Médicament comprenant comme ingrédient actif l'anticorps modifié de l'une quelconque des revendications 1 à 15.

20. Utilisation de l'anticorps modifié de l'une quelconque des revendications 1 à 15 pour la préparation d'un médicament pour traiter la thrombocytopénie.

**21.** Procédé de criblage d'un anticorps modifié comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L d'un anticorps et montrant une action agoniste par réticulation d'un récepteur TPO, dans lequel l'anticorps modifié est:

- (i) un multimère d'une simple chaîne Fv comprenant une région V d'une chaîne H et une région V d'une chaîne L; ou  
(ii) un polypeptide à simple chaîne comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L,

qui comprend les étapes de

- (1) produire un anticorps modifié comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L d'un anticorps et se liant spécifiquement à un récepteur TPO,  
(2) exposer des cellules exprimant ledit récepteur TPO à réagir avec l'anticorps modifié et  
(3) mesurer une action agoniste TPO dans les cellules causée par réticulation d'un récepteur TPO.

**22.** Procédé de mesure d'une action agoniste d'un anticorps modifié comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L d'un anticorps et montrant une action agoniste par réticulation d'un récepteur TPO, dans lequel l'anticorps modifié est:

- (i) un multimère d'une simple chaîne Fv comprenant une région V d'une chaîne H et une région V d'une chaîne L; ou  
(ii) un polypeptide à simple chaîne comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L,

qui comprend les étapes de

- (1) produire un anticorps modifié comprenant deux ou davantage de régions V d'une chaîne H et deux ou davantage de régions V d'une chaîne L d'un anticorps et se liant spécifiquement à un récepteur TPO,  
(2) exposer des cellules exprimant ledit récepteur TPO à réagir avec l'anticorps modifié et  
(3) mesurer une action agoniste TPO dans les cellules causée par réticulation d'un récepteur TPO.

**23.** Anticorps modifié de l'une quelconque des revendications 1 à 15 pour une utilisation dans un procédé de traitement de la thrombocytopénie.

Fig. 1

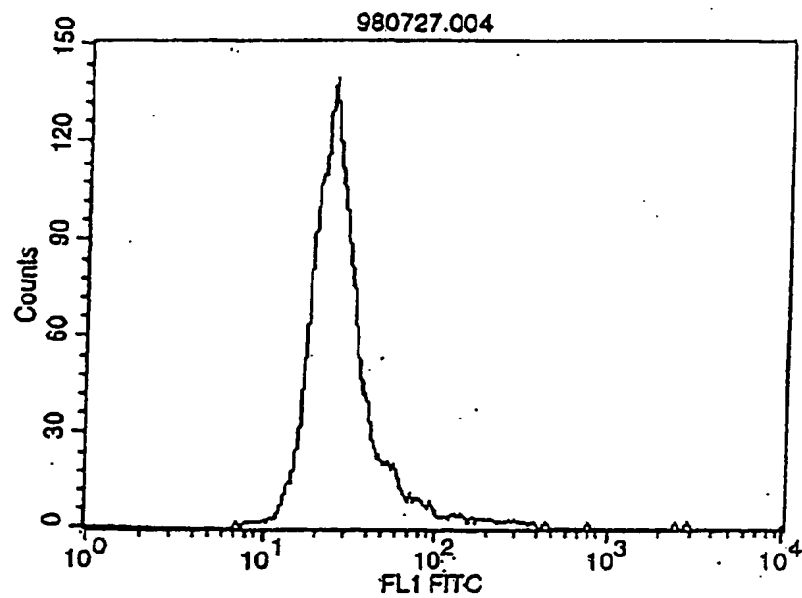


Fig. 2

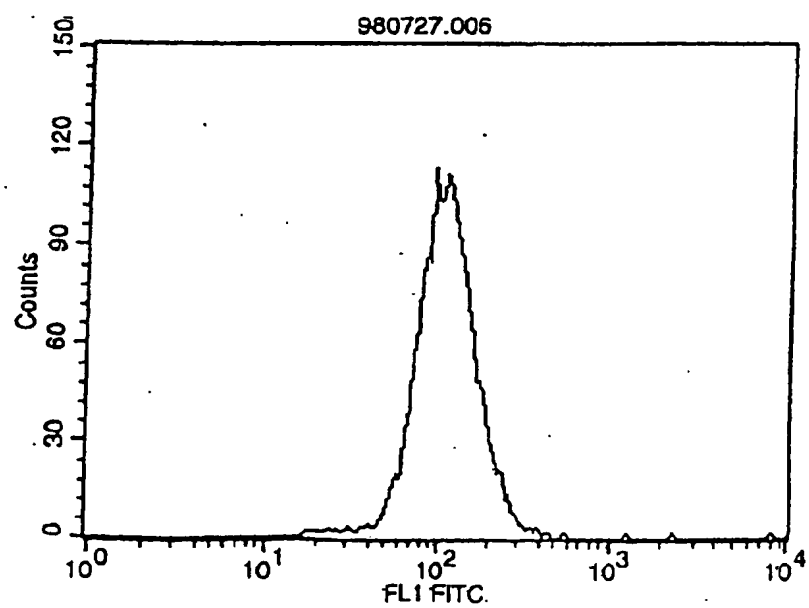


Fig. 3

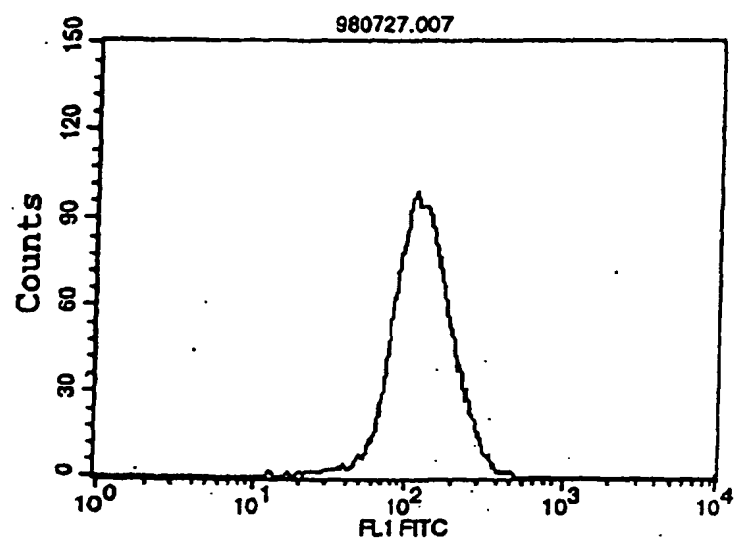


Fig. 4

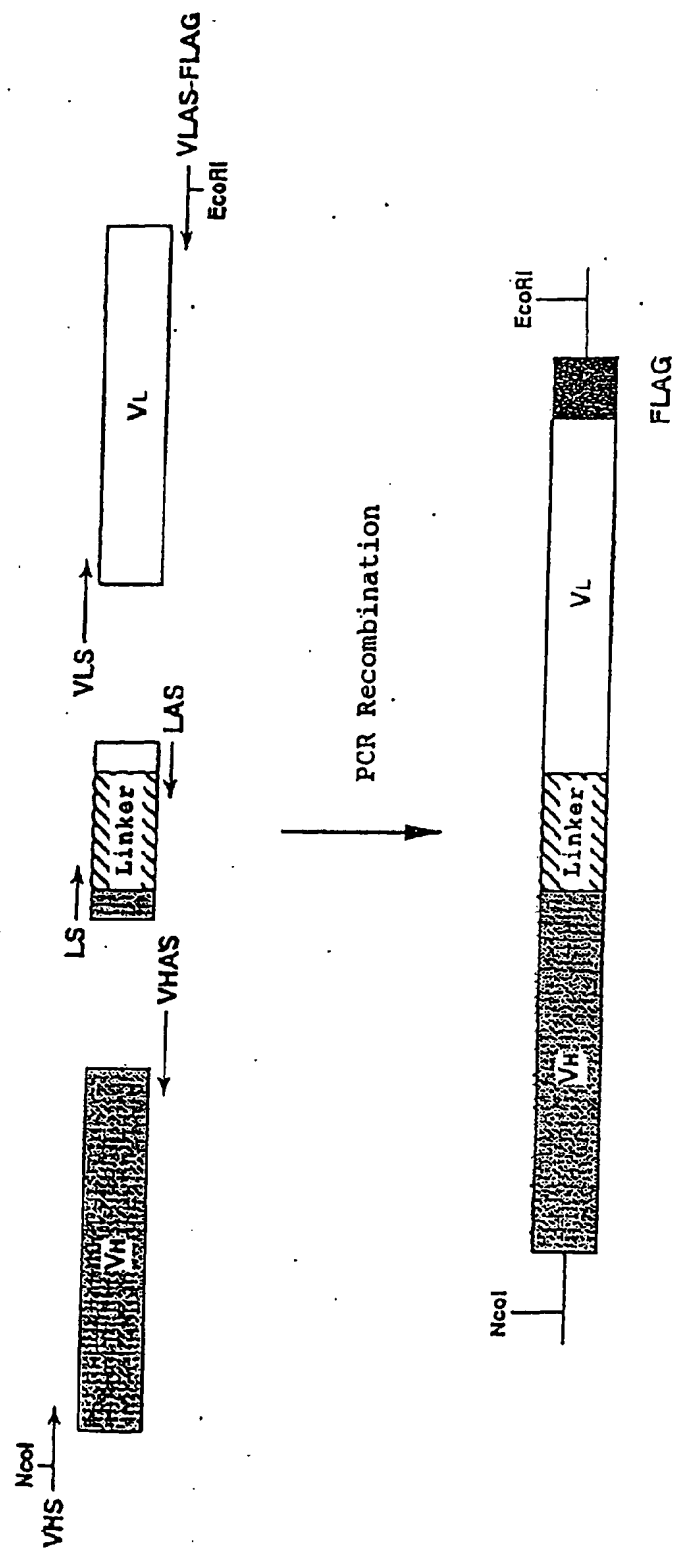


Fig. 5

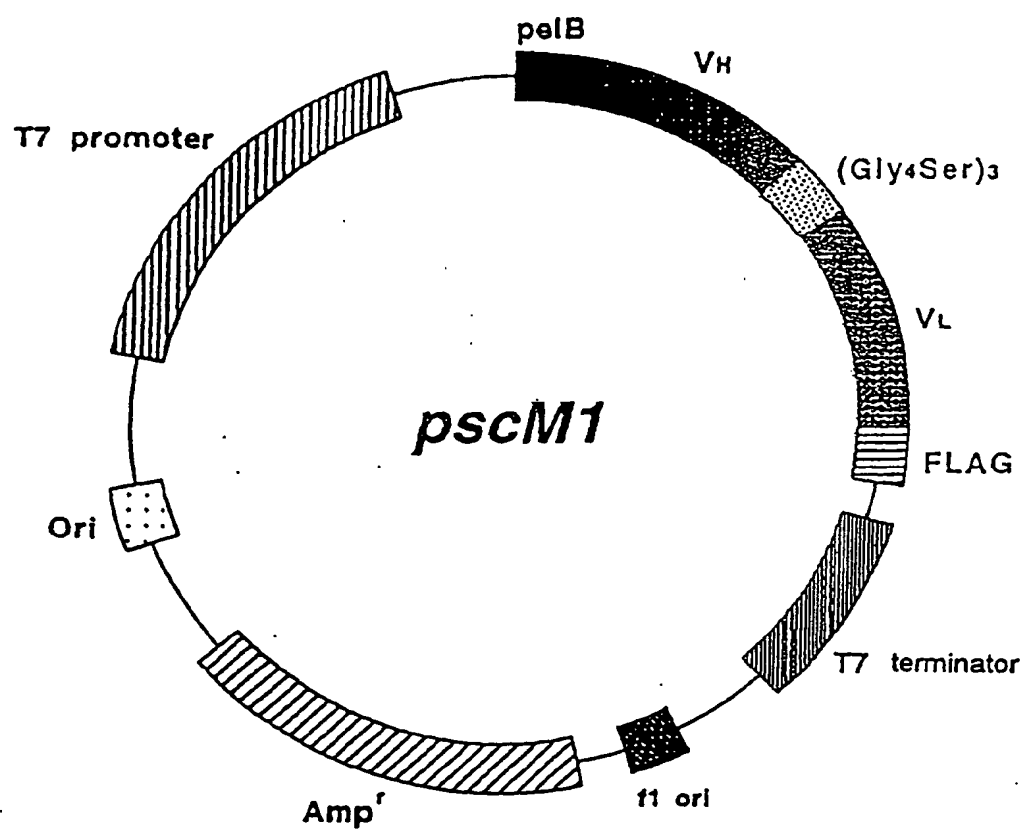
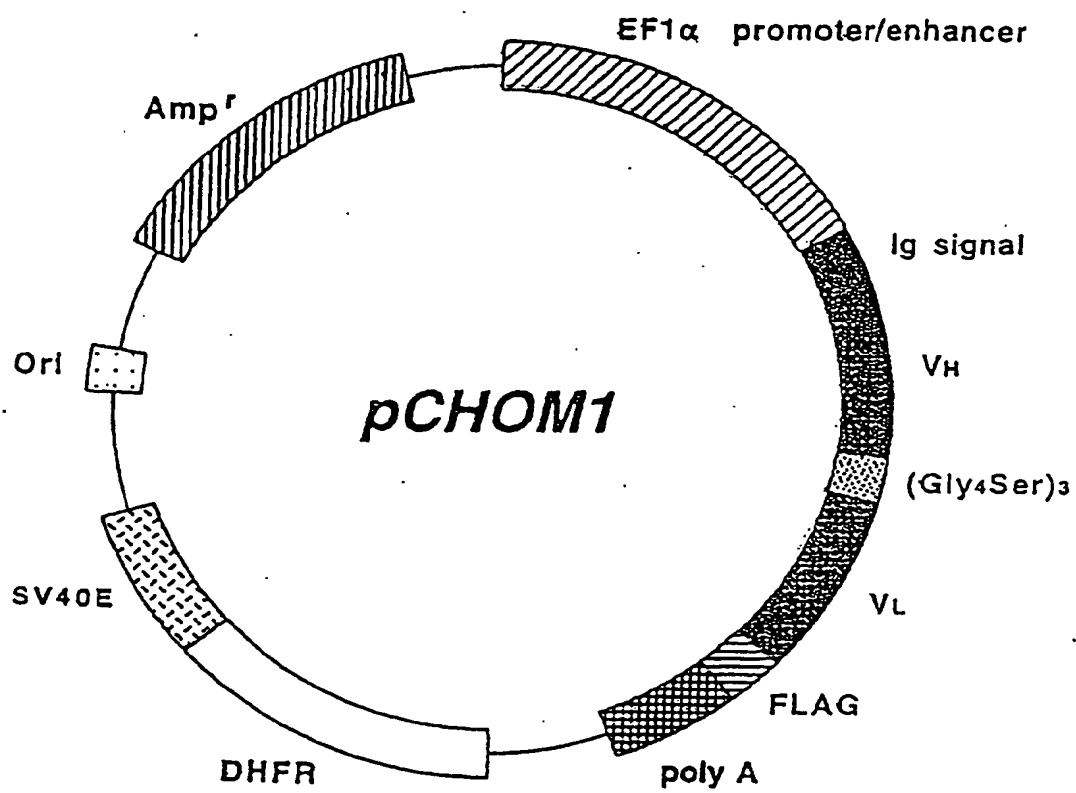


Fig. 6





**Fig. 7**

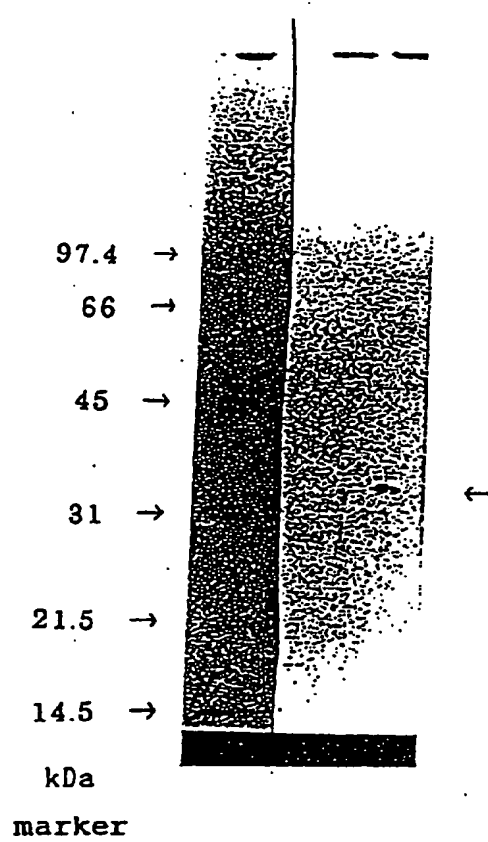


Fig. 8

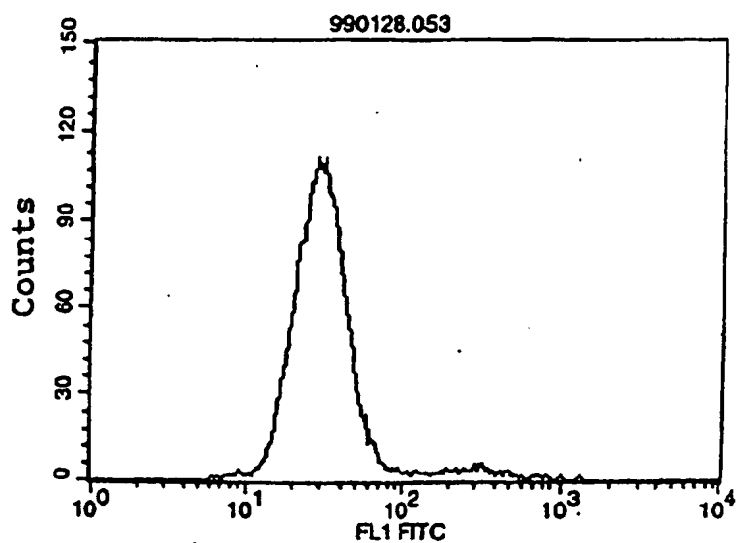


Fig. 9

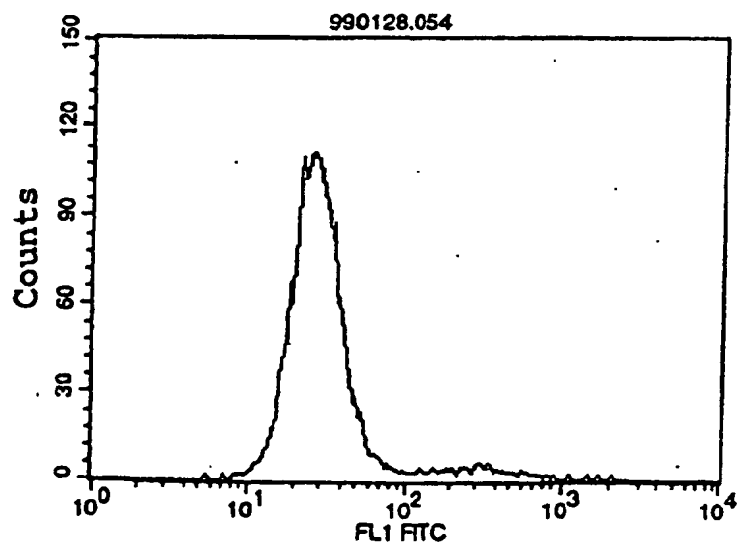


Fig. 10

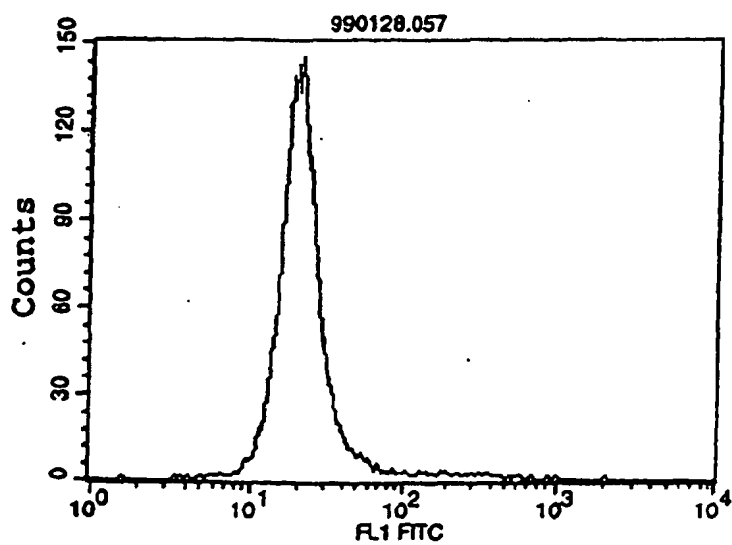


Fig. 11

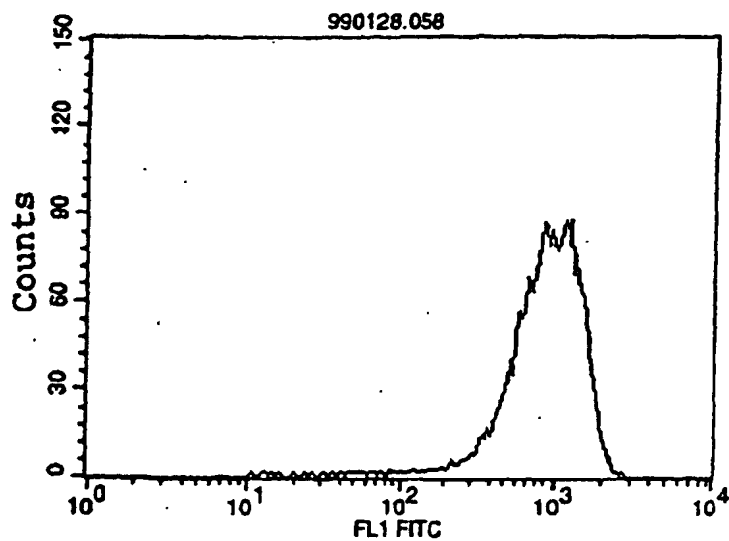


Fig. 12

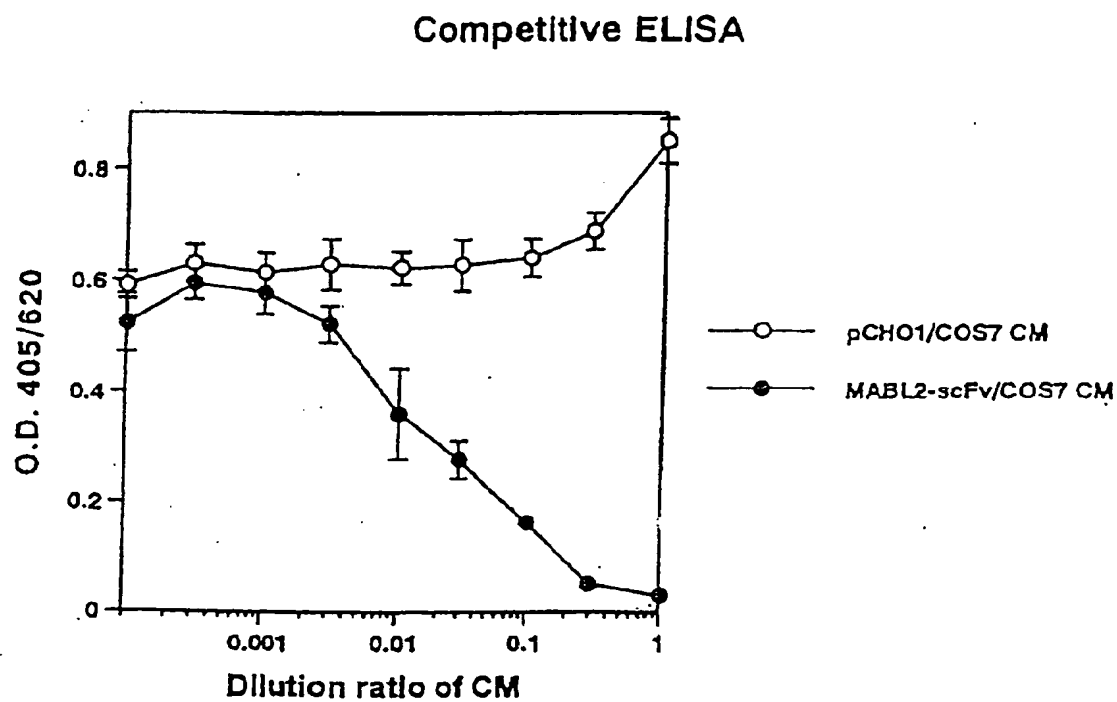


Fig. 13

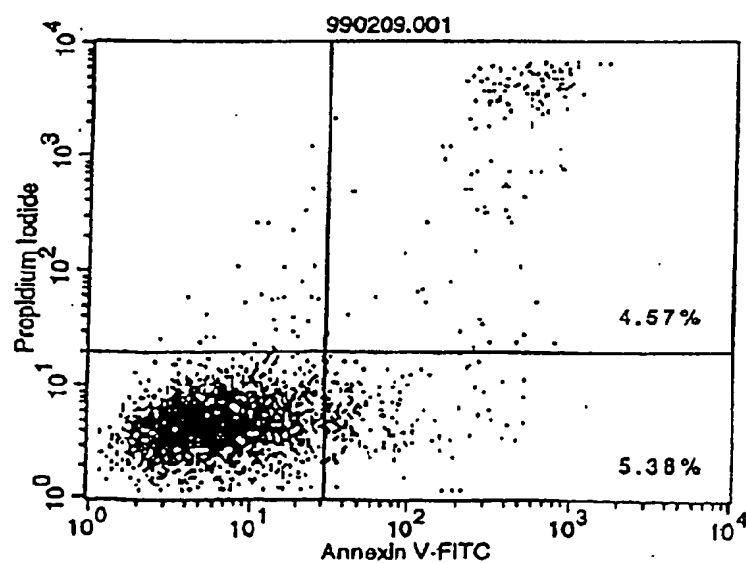


Fig. 14

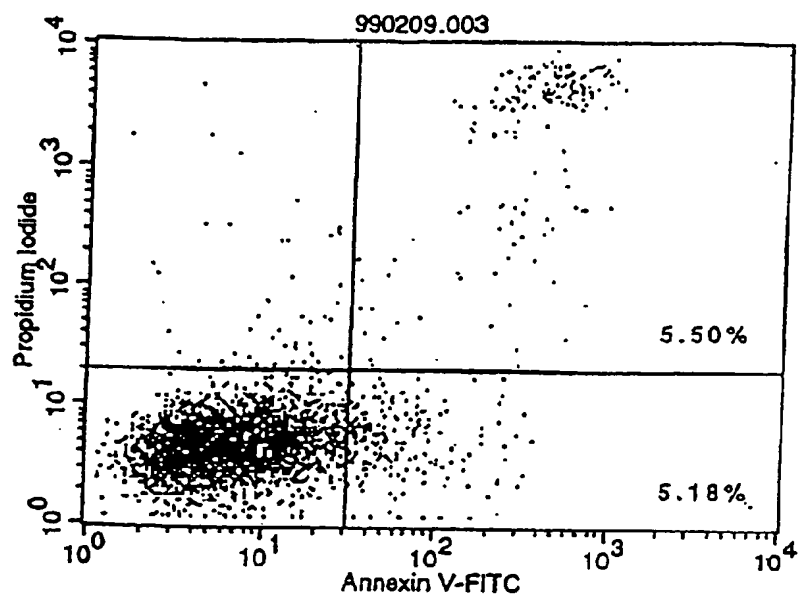


Fig. 15

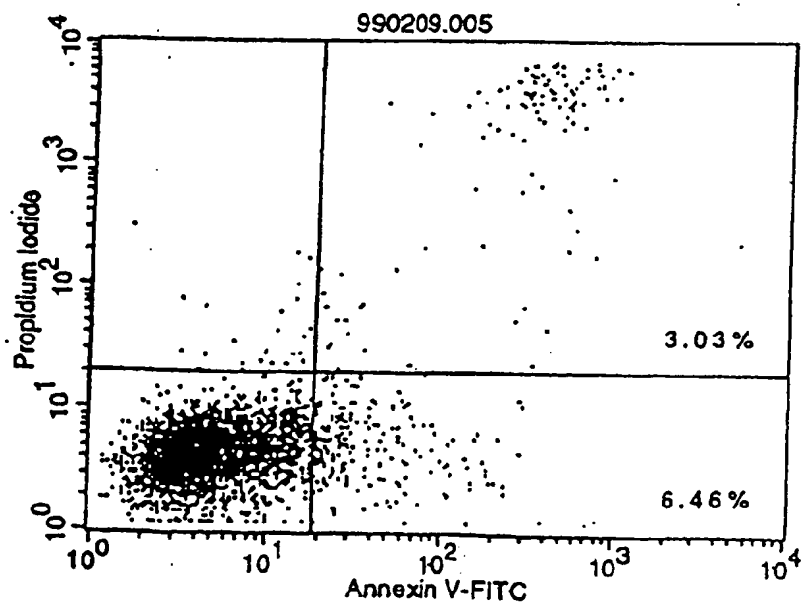


Fig. 16

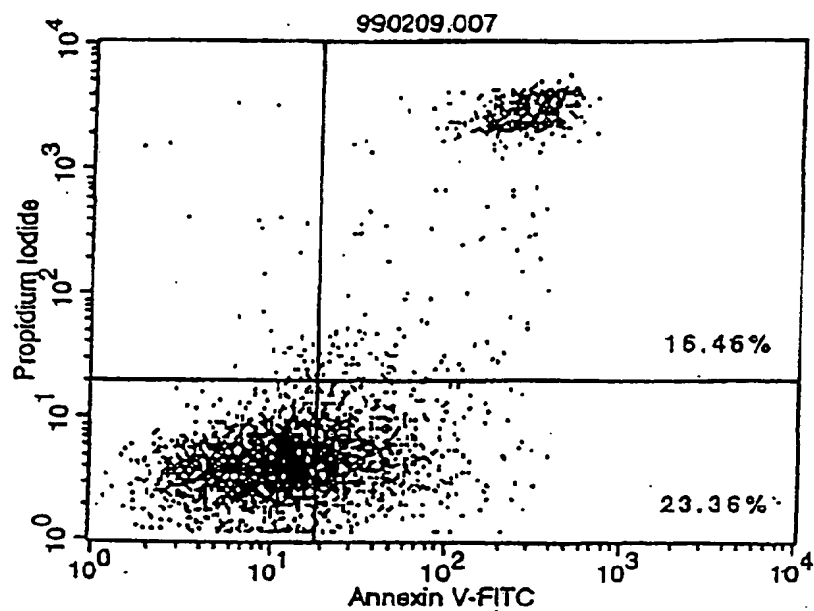


Fig. 17

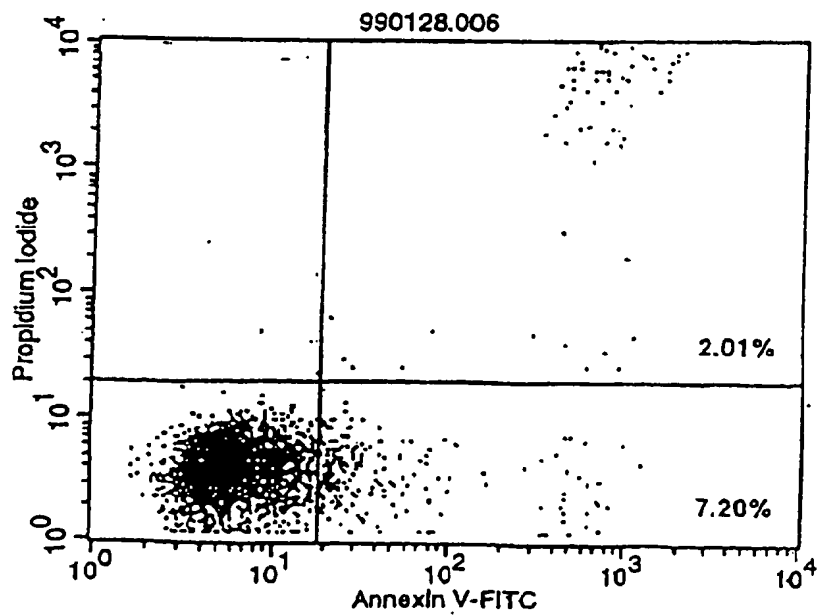


Fig. 18

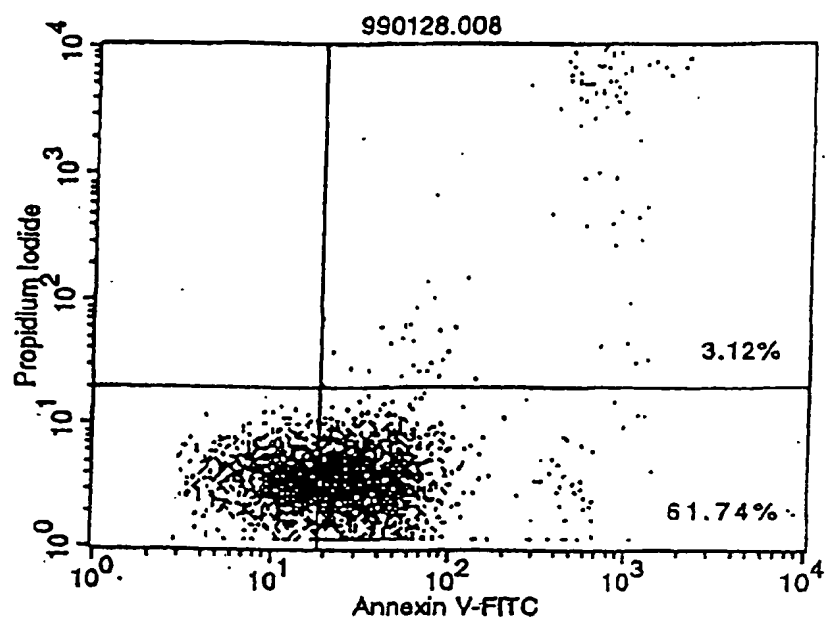


Fig. 19

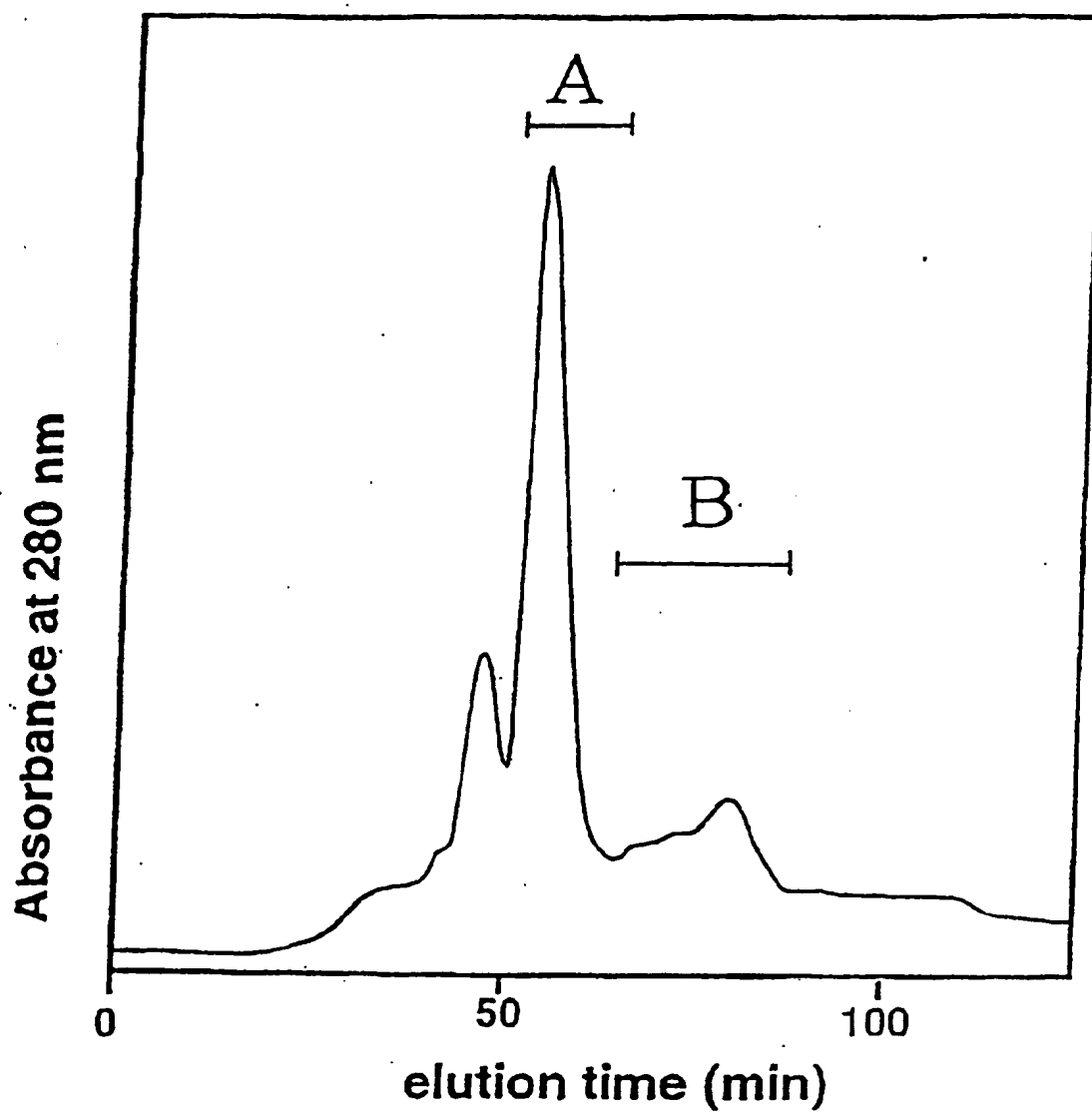




Fig. 20

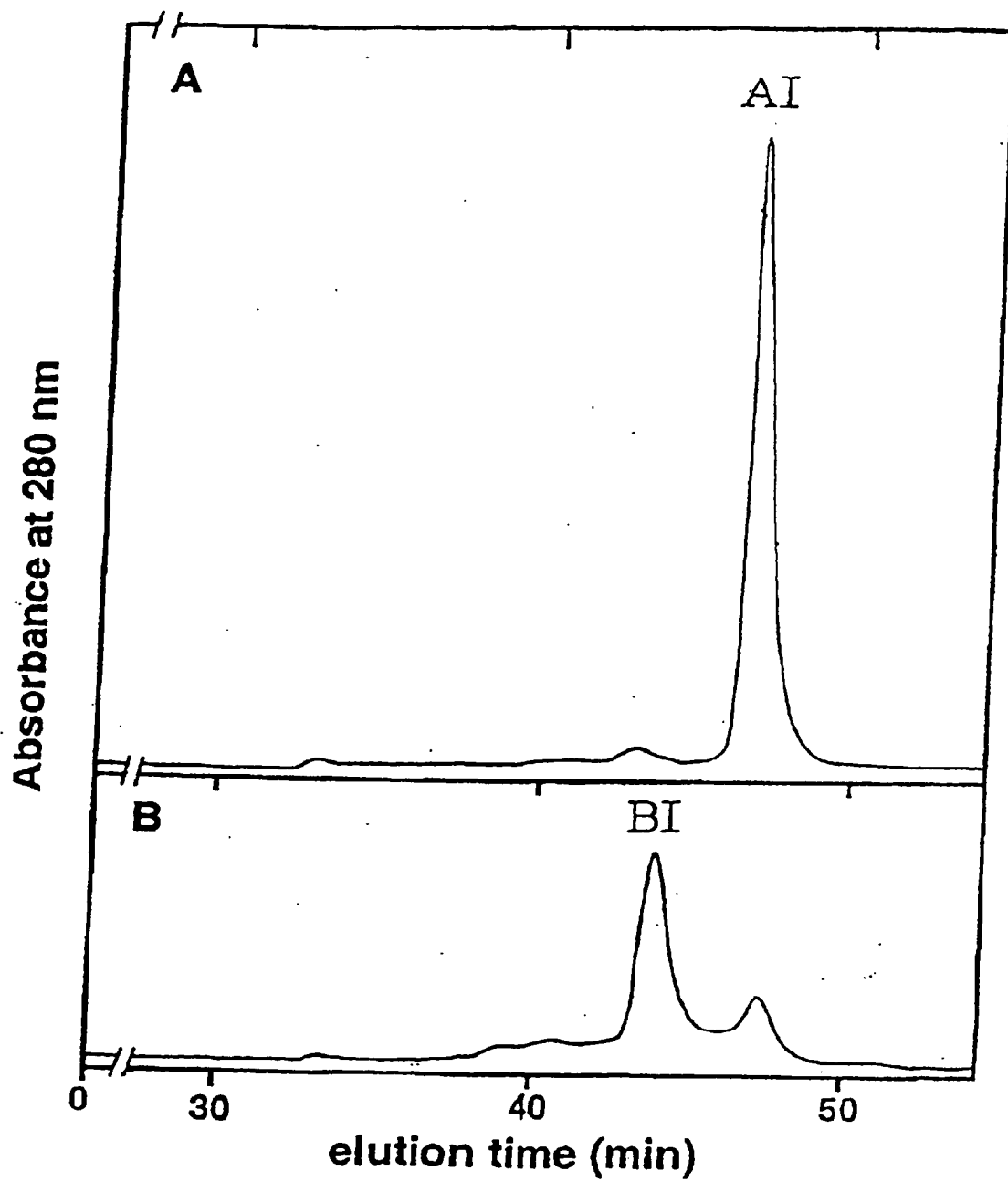
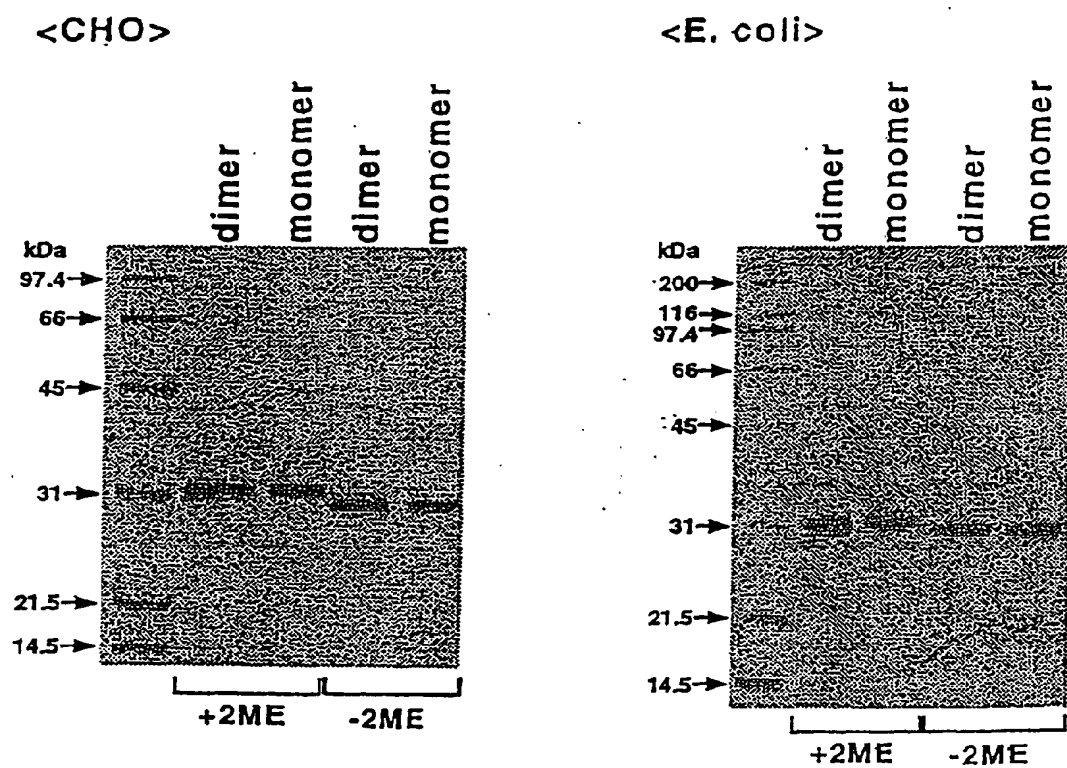


Fig. 21

SDS-PAGE analysis of MABL2-scFv



**Fig. 22**

TSK gel G3000SW

20 mM Acetate buffer, 0.15 M NaCl, pH 6.0

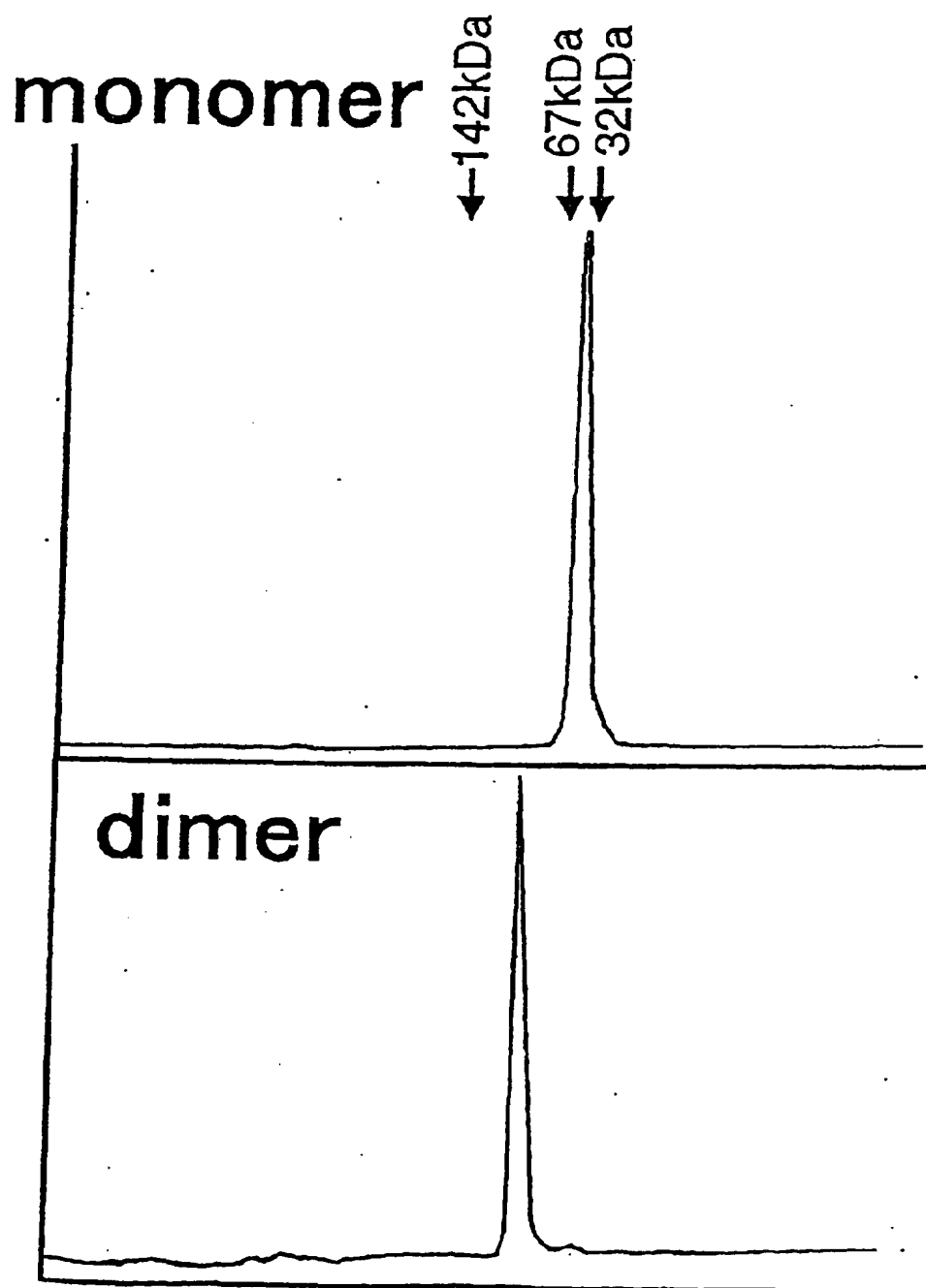


Fig. 23

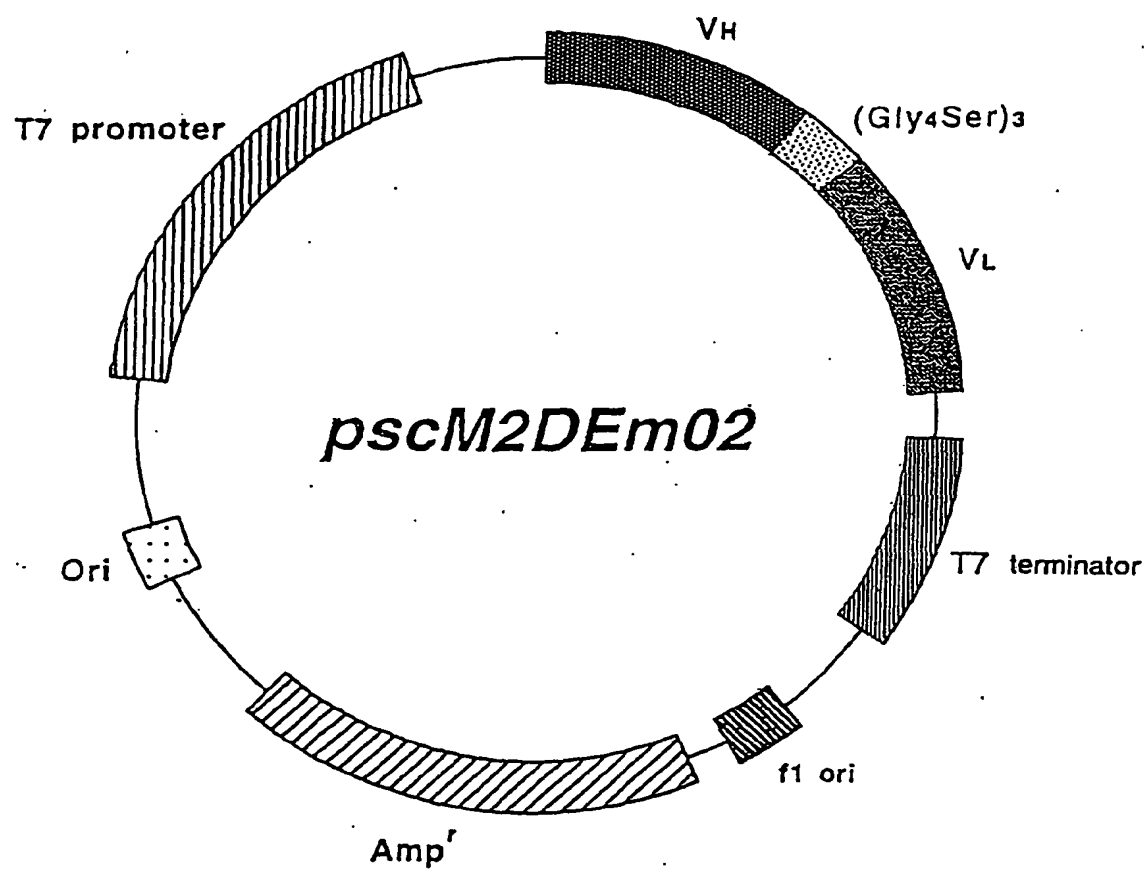


Fig. 24

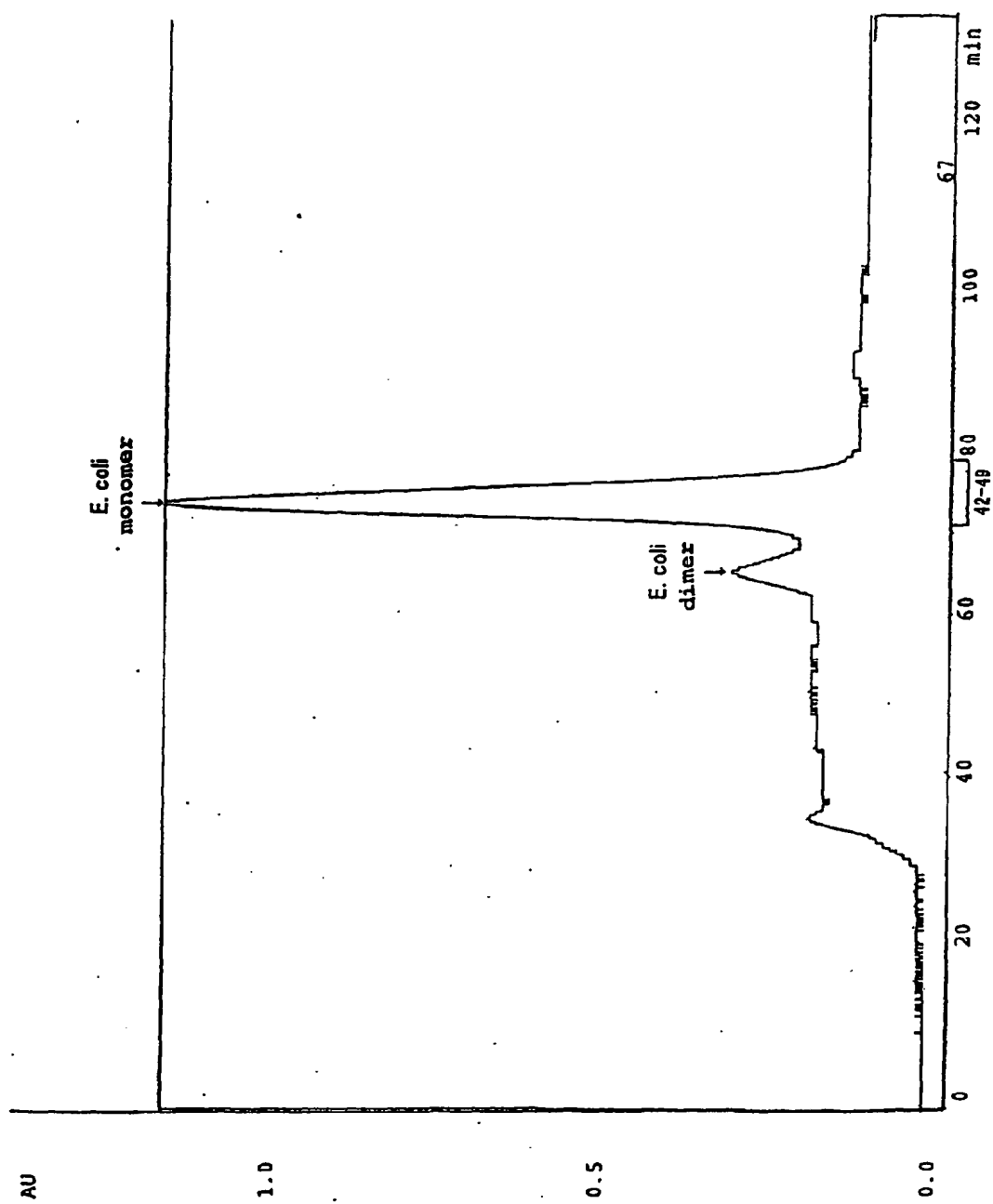


Fig. 25

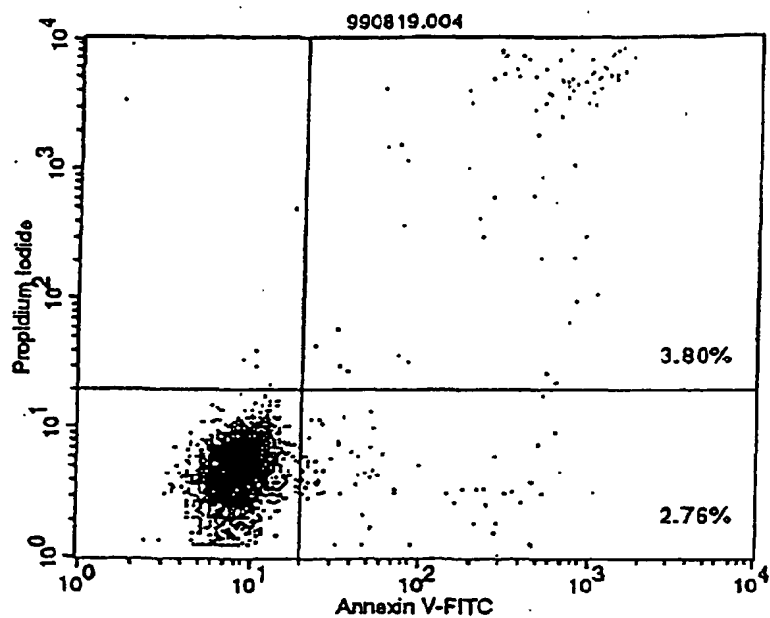


Fig. 26

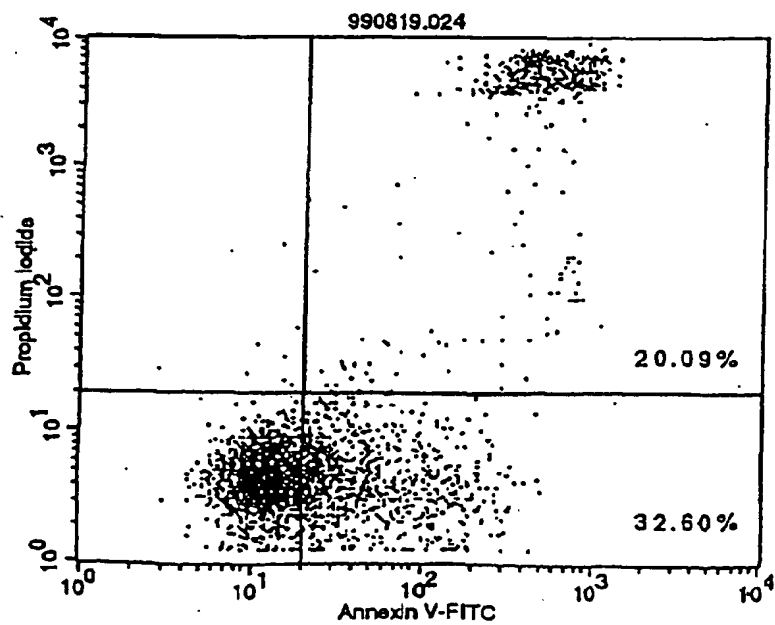


Fig. 27

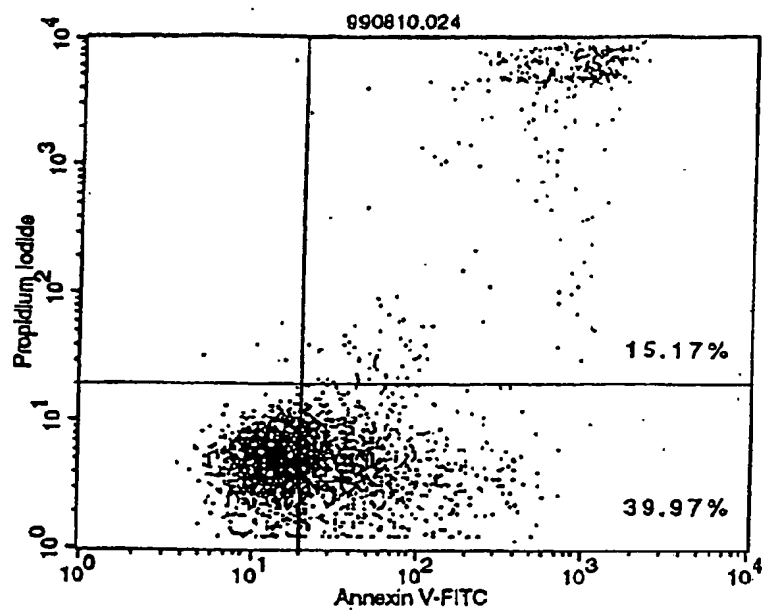


Fig. 28

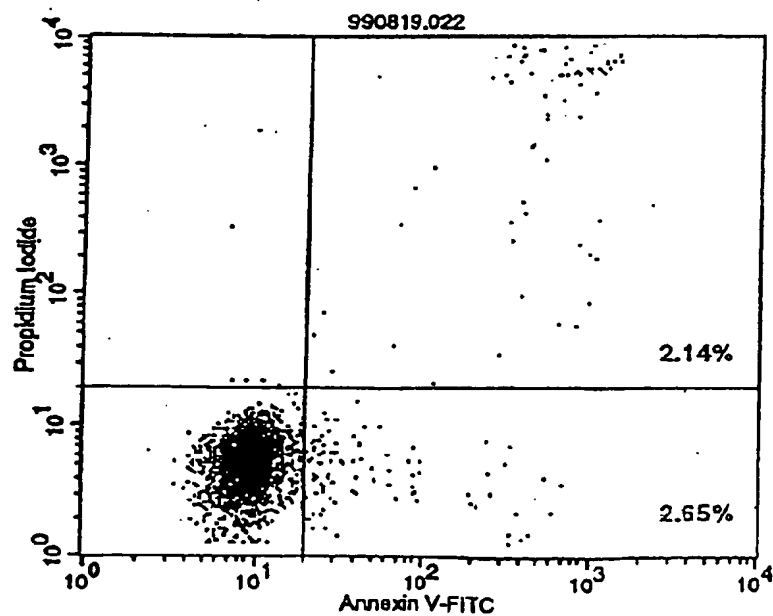


Fig. 29

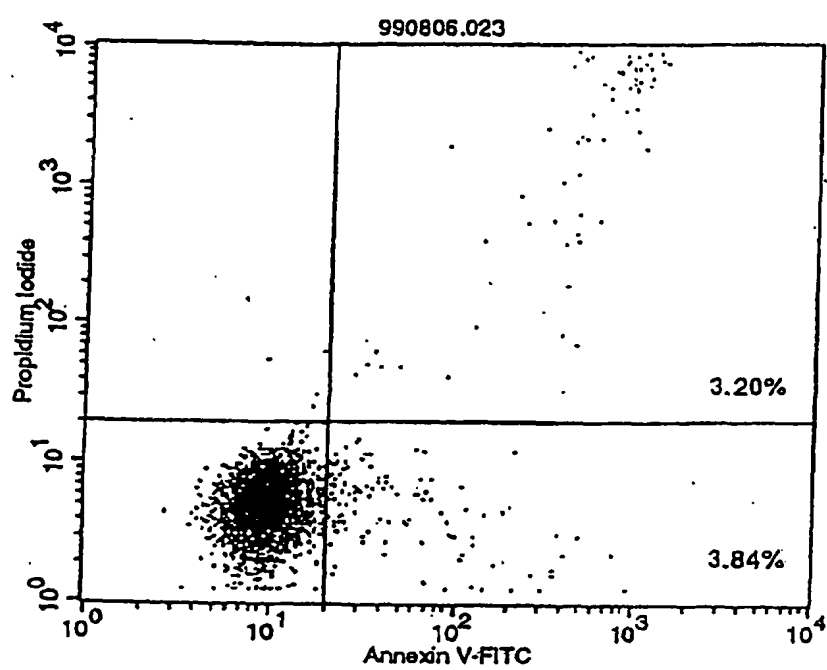




Fig. 30

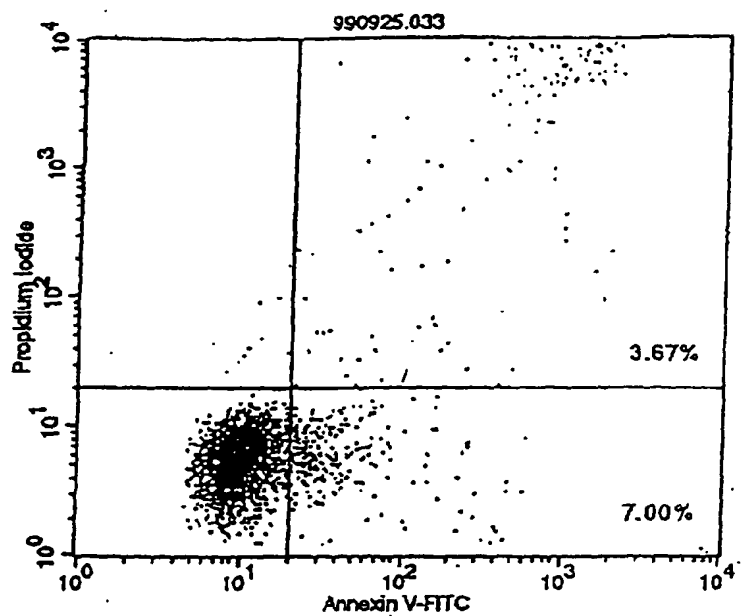


Fig. 31

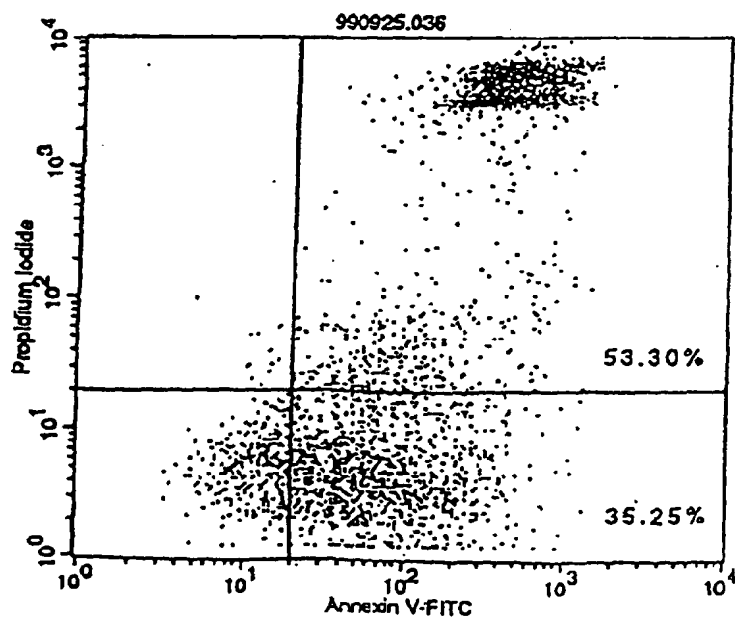


Fig. 32

*Effect of MABL-2 (scFv) on serum hlgG  
in KPMM2 i.v. SCID mice*

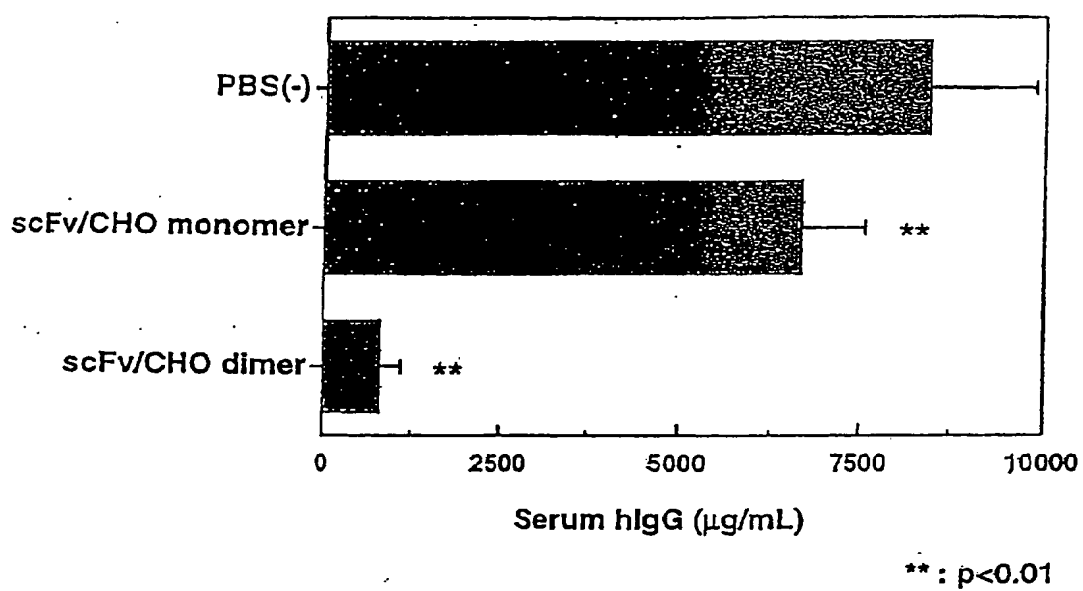


Fig. 33

*Effect of MABL-2 (scFv) on survival of KPMM2 i.v. SCID mice*

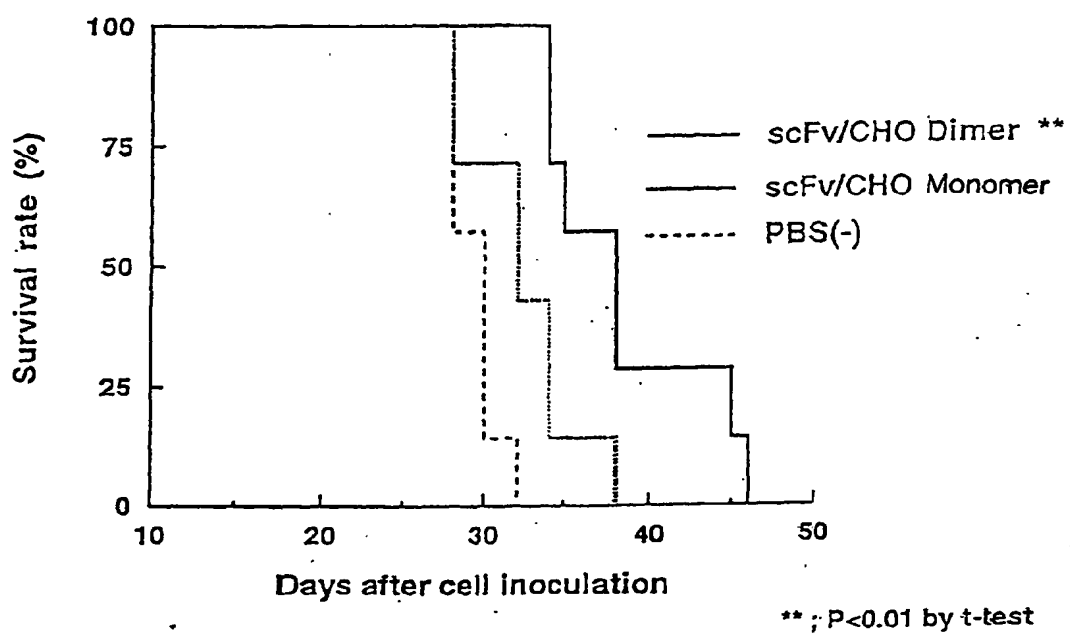


Fig. 34

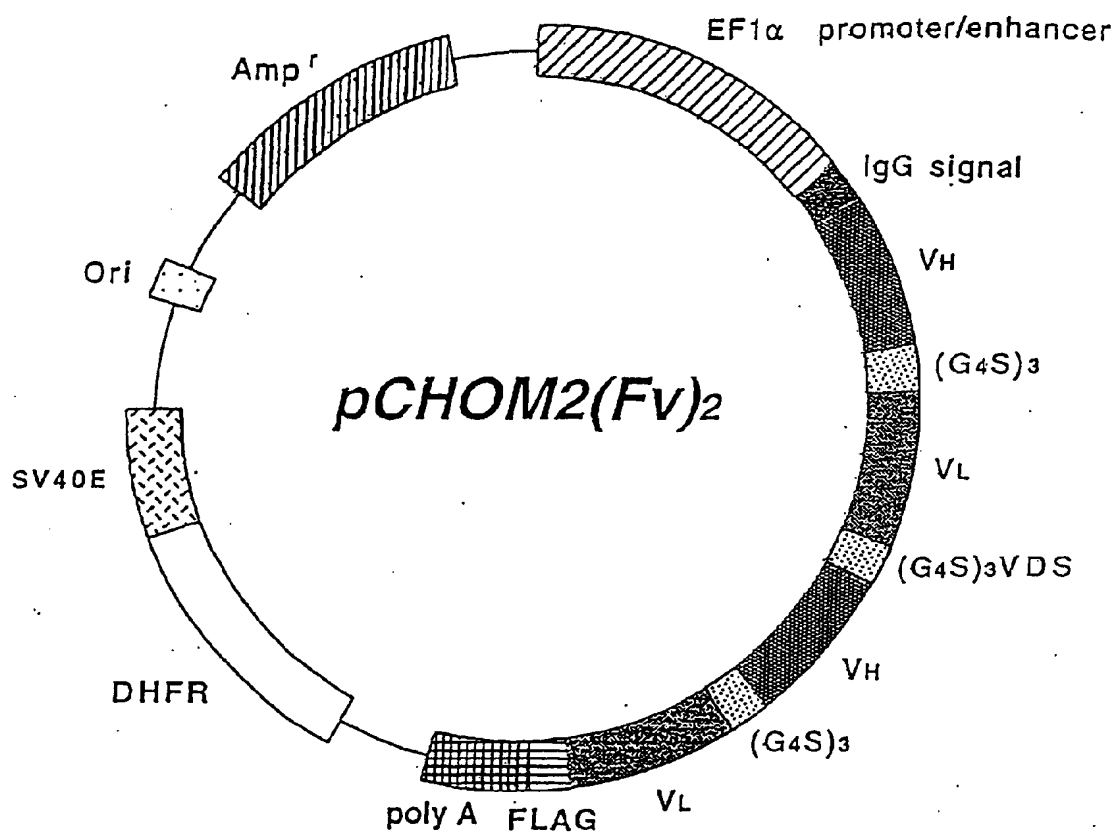


Fig. 35

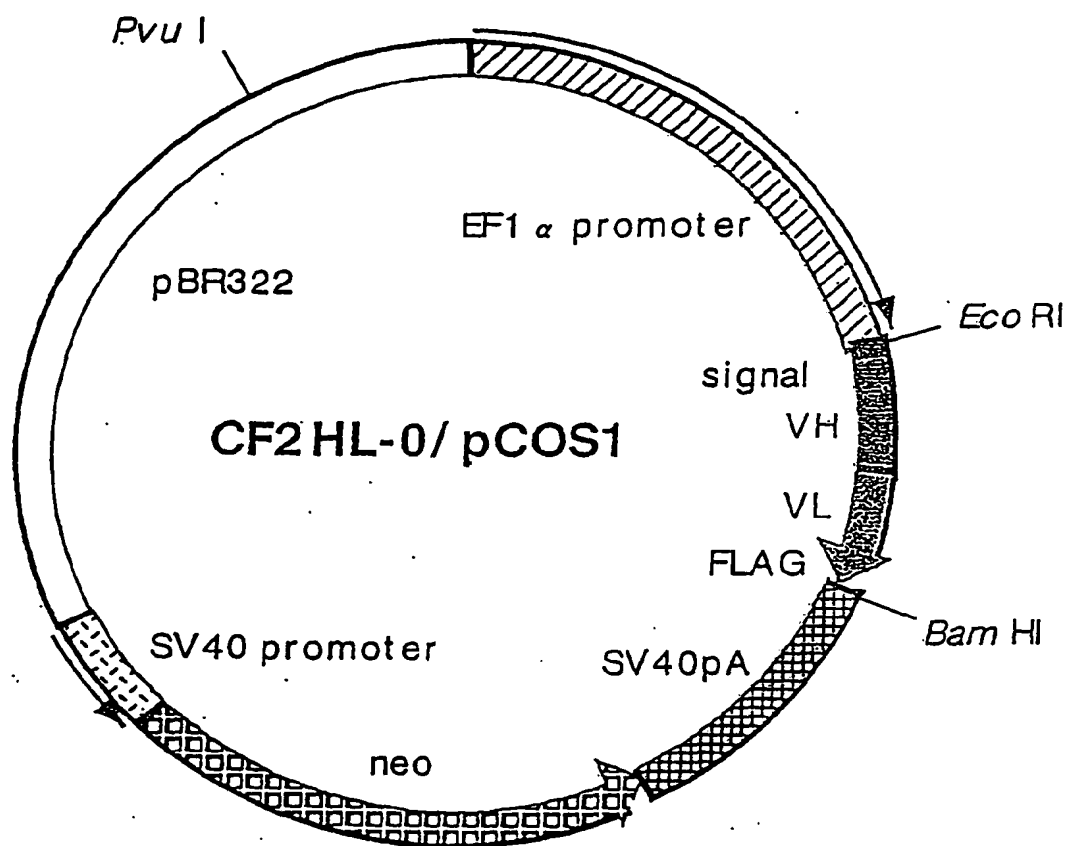
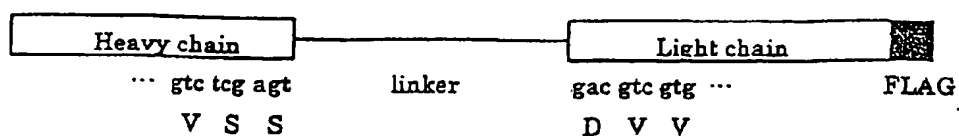


Fig. 36

## Base Sequence and Amino Acid Sequence of Linker for HL Type



Plasmid	Number of linker amino acid	linker	
CF2HL-0/pCOS1	0	gtc tcg agt V S S	gac gtc gtg D V V
CF2HL-3/pCOS1	3	gtc tcg agt ggt ggt tcc V S S G G S	gac gtc gtg D V V
CF2HL-4/pCOS1	4	gtc tcg agt ggt ggt ggt tcc V S S G G G S	gac gtc gtg D V V
CF2HL-5/pCOS1	5	gtc tcg agt ggt ggt ggt ggt tcc V S S G G G G S	gac gtc gtg D V V
CF2HL-6/pCOS1	6	gtc tcg agt gt ggt ggt ggt ggt tcc V S S G G G G G S	gac gtc gtg D V V
CF2HL-7/pCOS1	7	gtc tcg agt ggt ggt ggt ggt ggt ggt tcc V S S G G G G G G S	gac gtc gtg D V V

Fig. 37

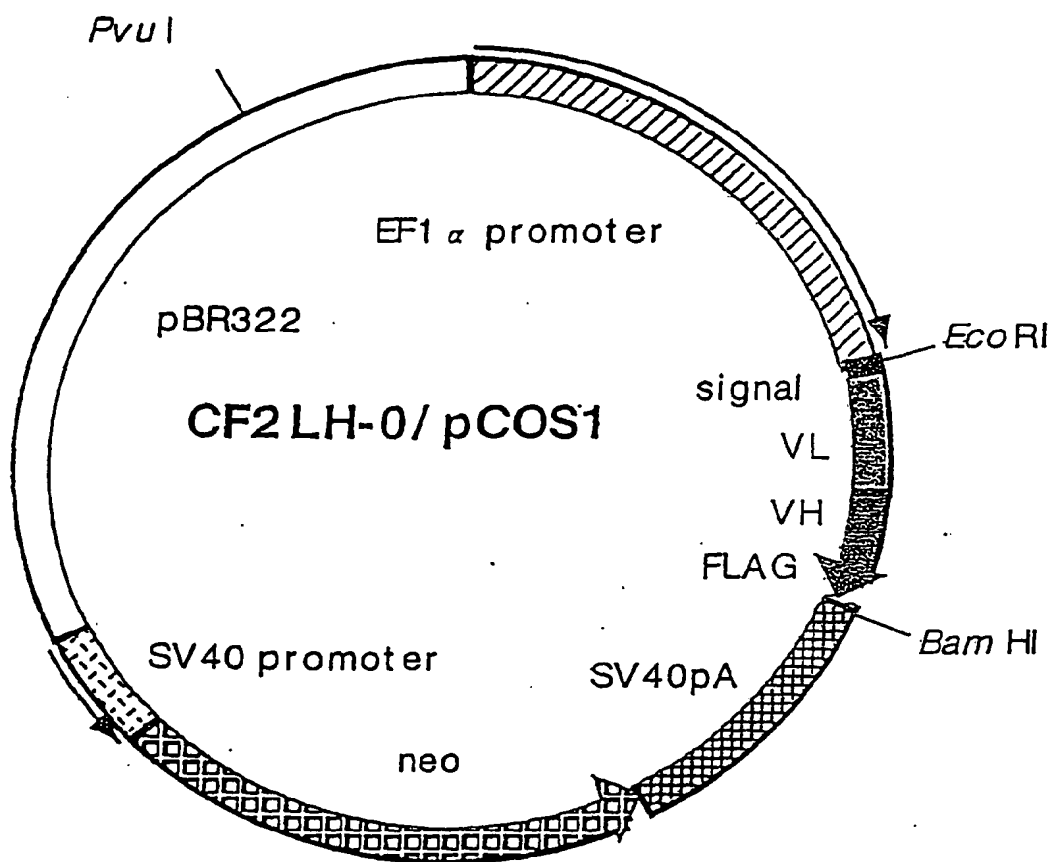


Fig. 38

## Base Sequence and Amino Acid Sequence of Linker for LH Type

Light chain		Heavy chain	
...	gag ata aaa	cag gtc caa ...	FLAG
	E I K	Q V Q	
linker			
Plasmid	Number of linker amino acid	linker	
CF2LH-0/pCOS1	0	gag ata aaa	cag gtc caa
		E I K	Q V Q
CF2LH-3/pCOS1	3	gag ata aaa tcc gga ggc	cag gtc caa
		E I K S G G	Q V Q
CF2LH-4/pCOS1	4	gag ata aaa tcc gga ggt ggc	cag gtc caa
		E I K S G G G	Q V Q
CF2LH-5/pCOS1	5	gag ata aaa tcc gga ggt ggt ggc	cag gtc caa
		E I K S G G G G	Q V Q
CF2LH-6/pCOS1	6	gag ata aaa tcc gga ggt ggt ggt ggc	cag gtc caa
		E I K S G G G G G	Q V Q
CF2LH-7/pCOS1	7	gag ata aaa tcc gga ggt ggt ggt ggt ggc	cag gtc caa
		E I K S G G G G G G	Q V Q



Fig. 39

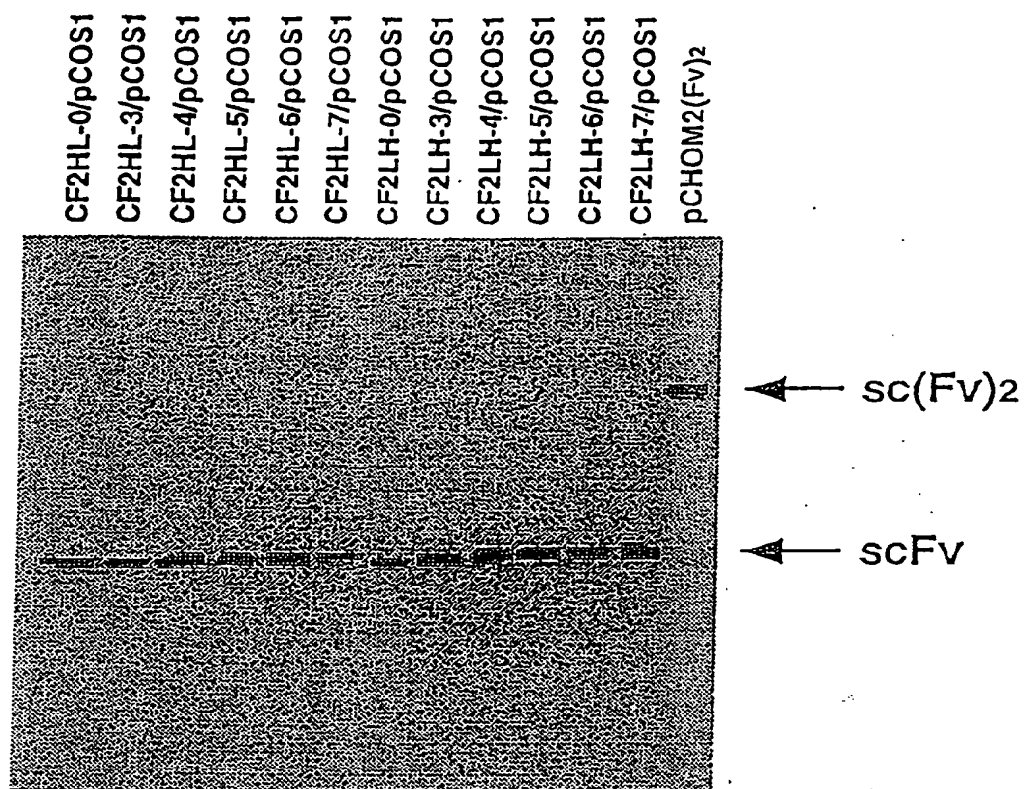


Fig. 40a

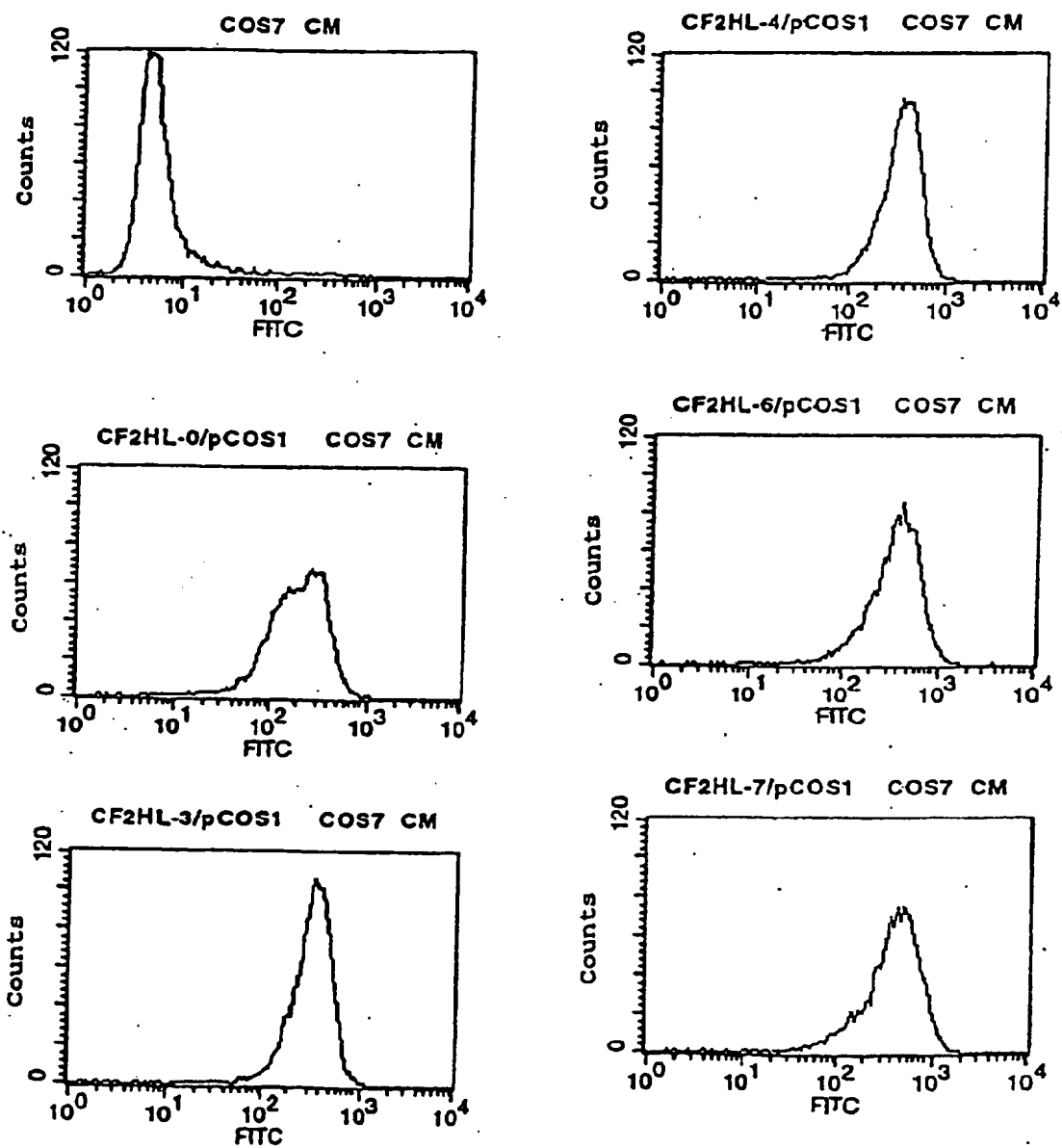


Fig. 40b

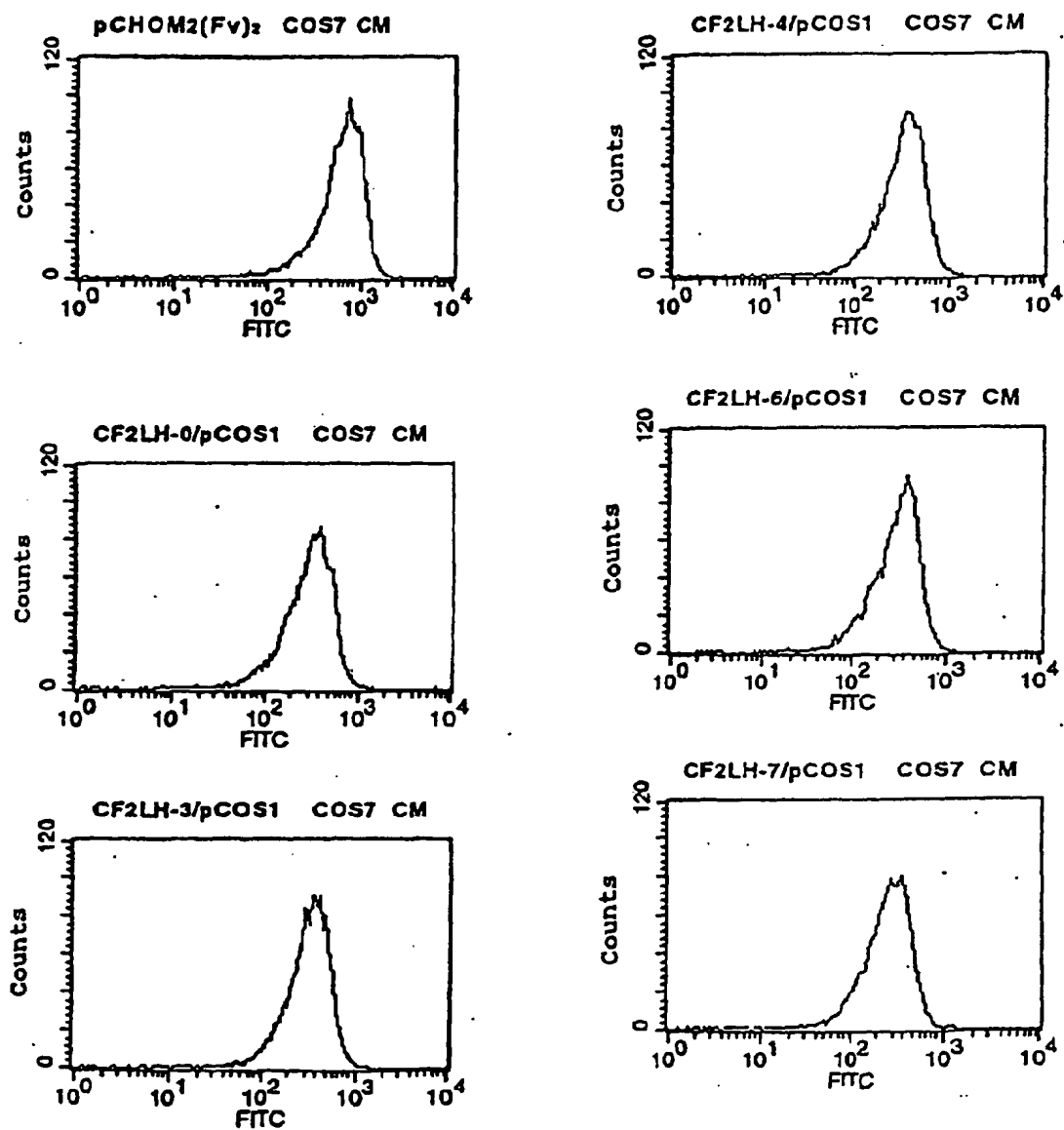


Fig. 41a

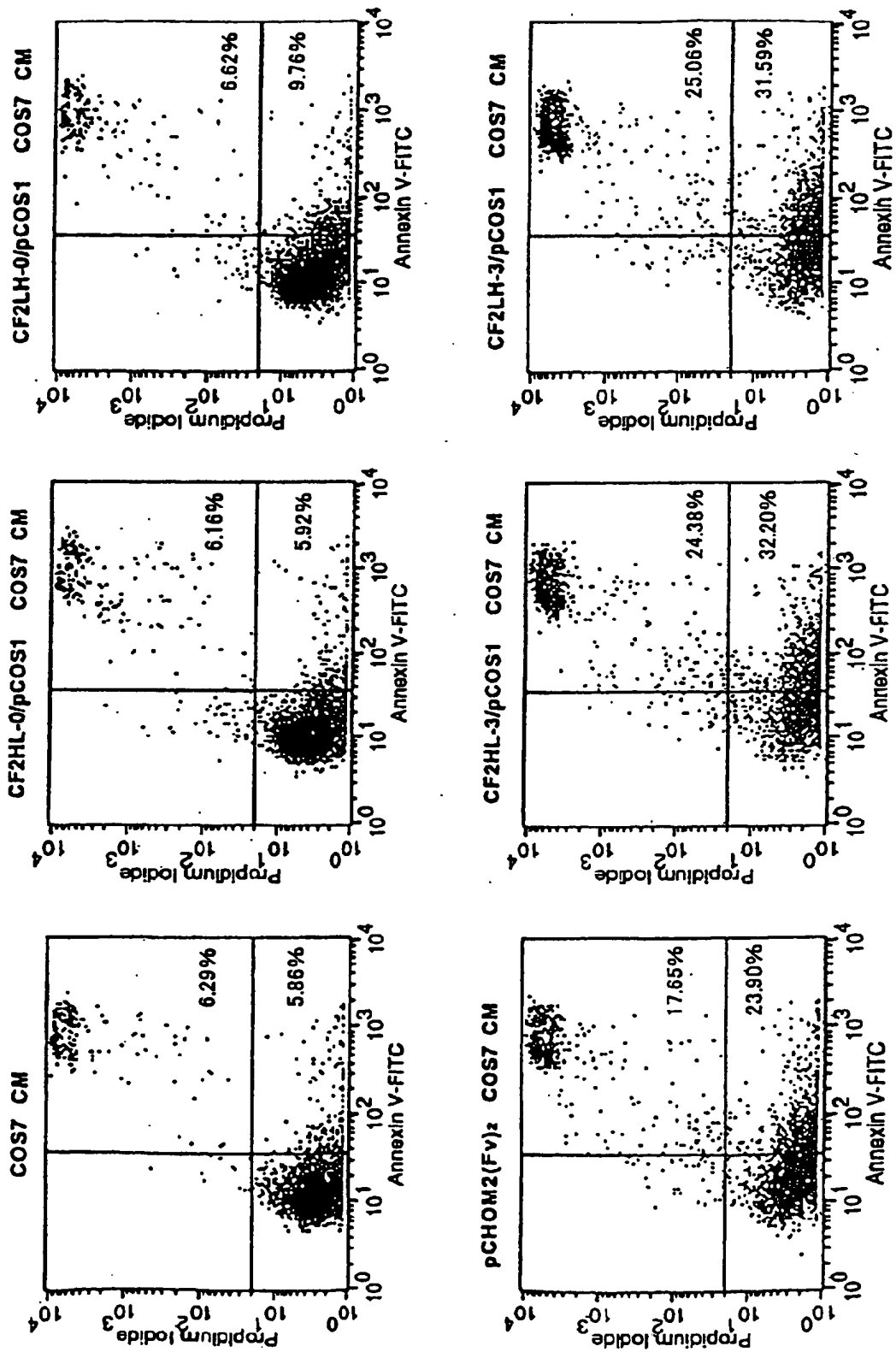


Fig. 41b

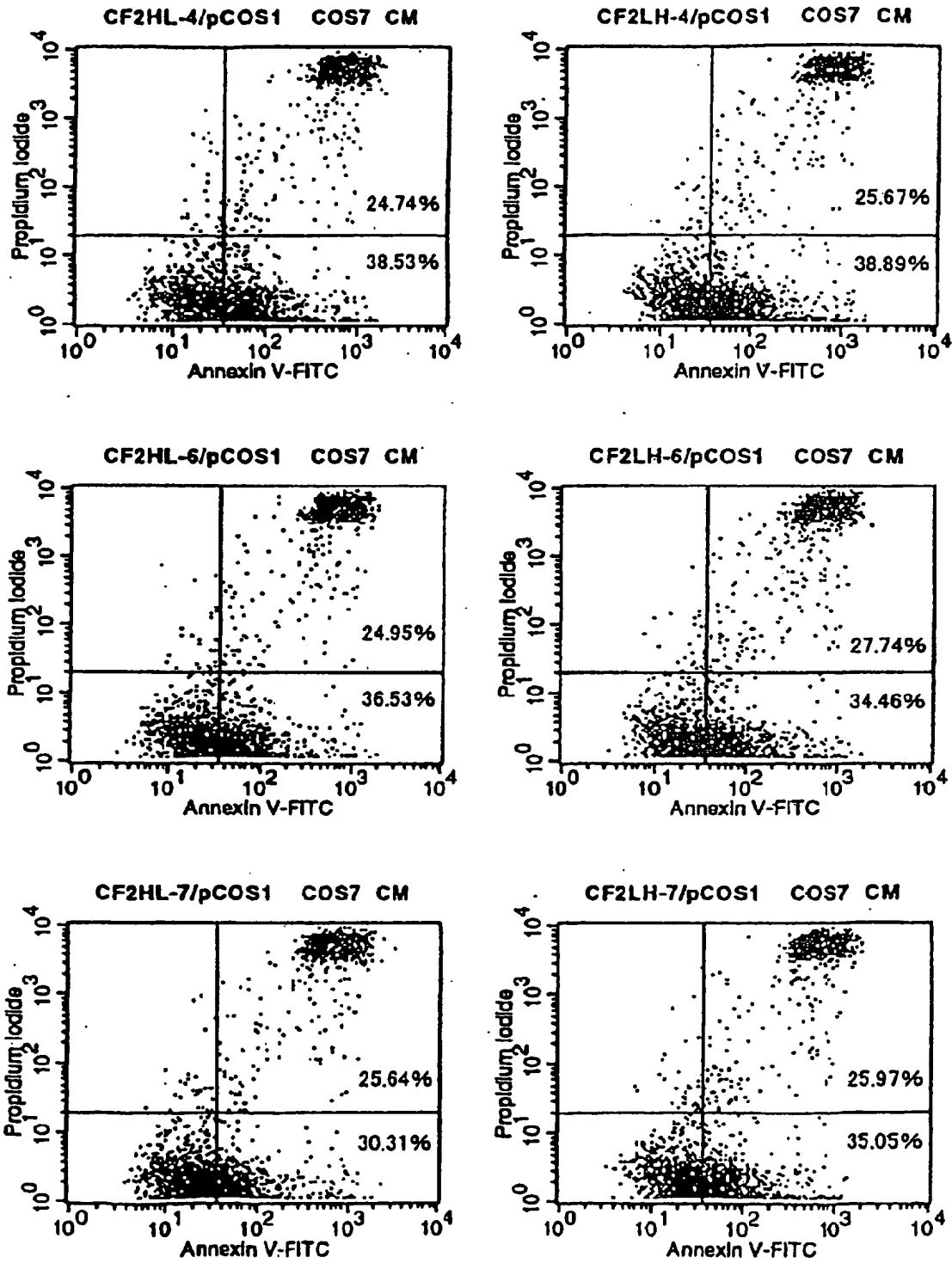


Fig. 42

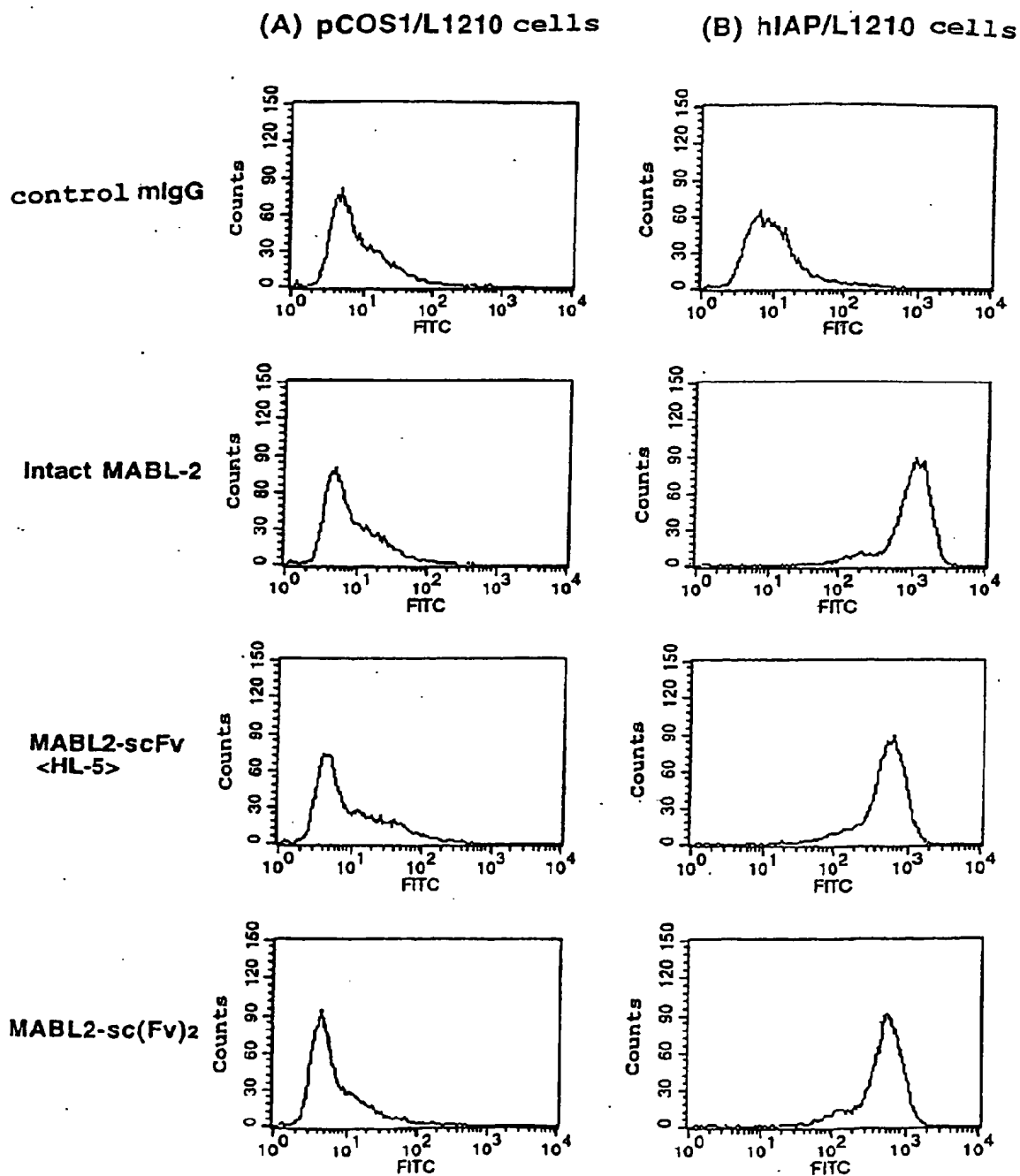


Fig. 43

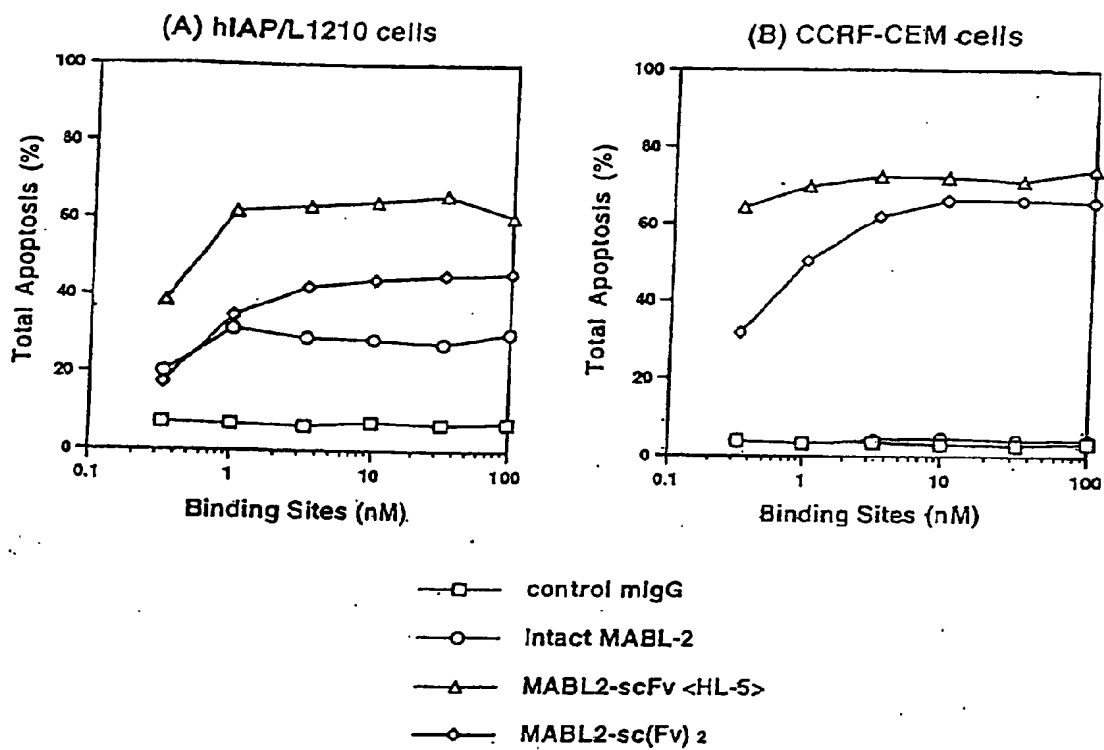


Fig. 44

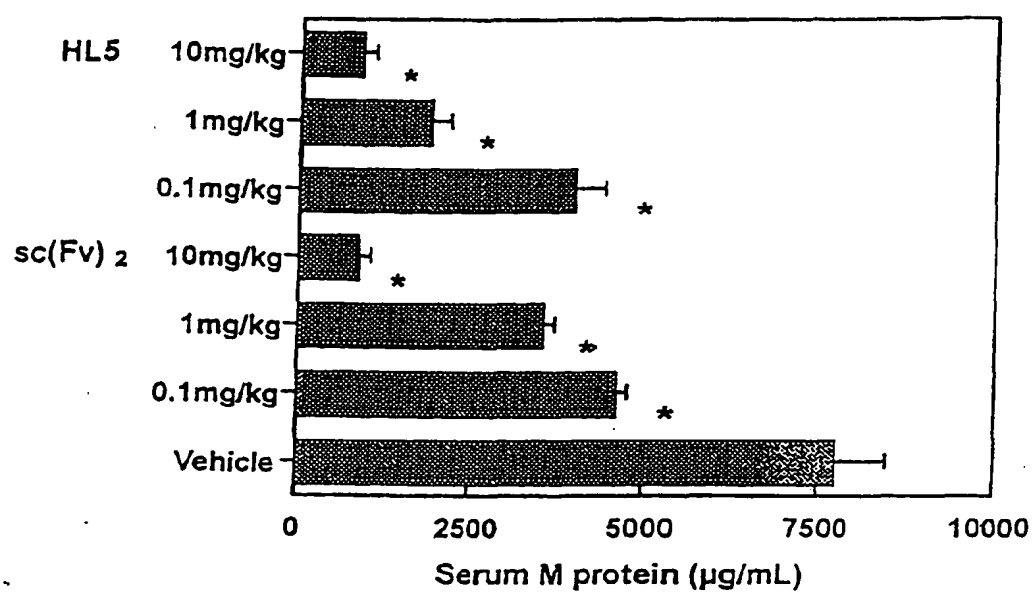




Fig. 45

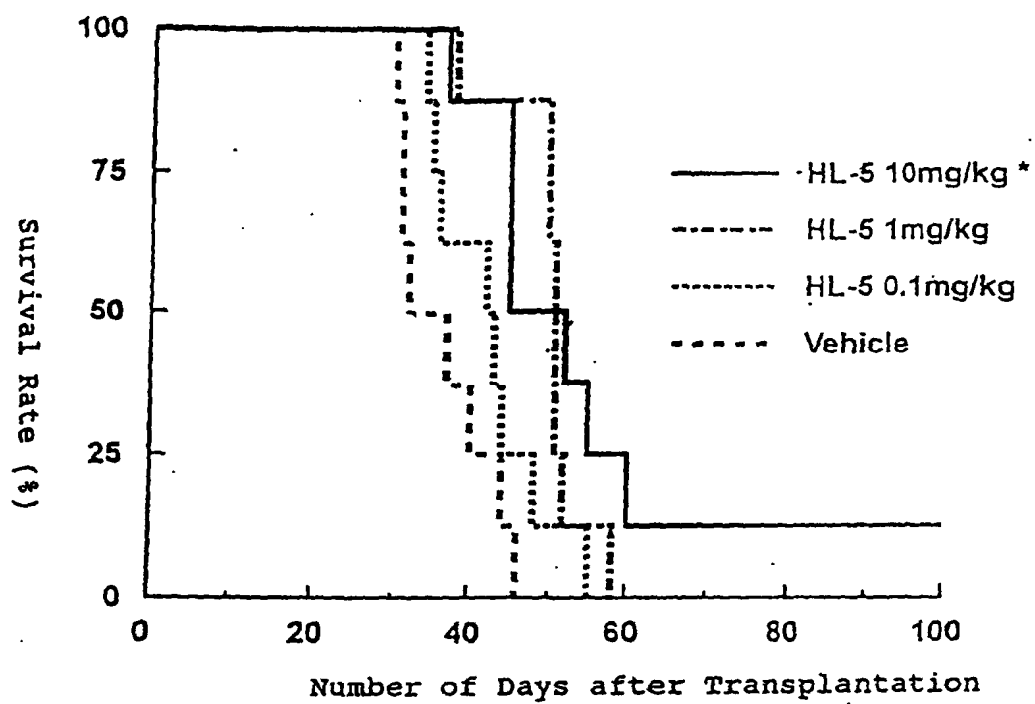


Fig. 46

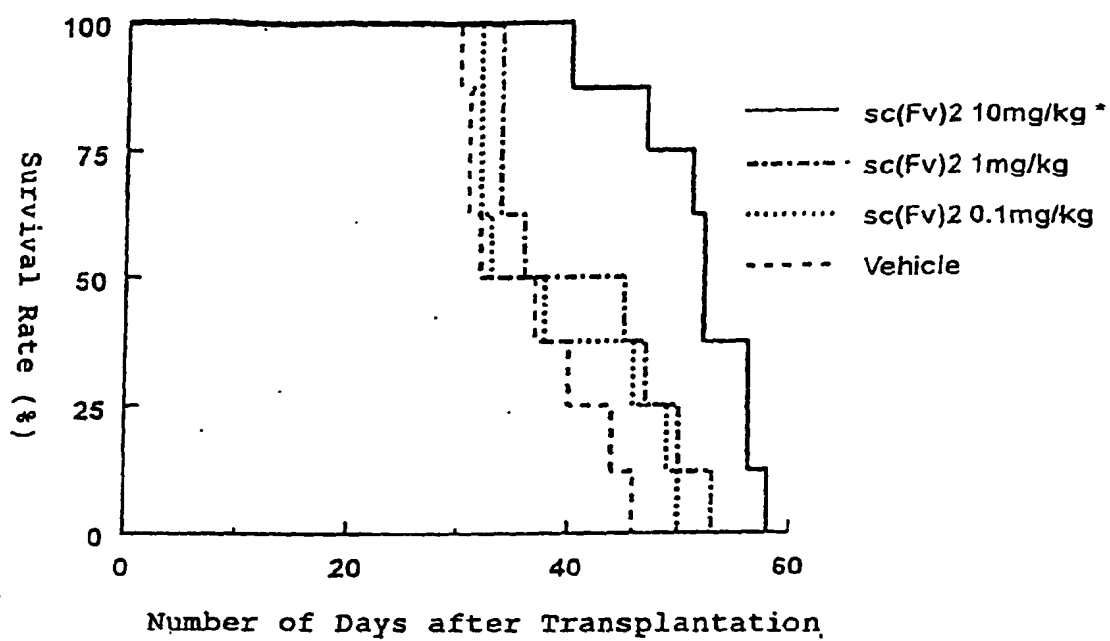


Fig. 47

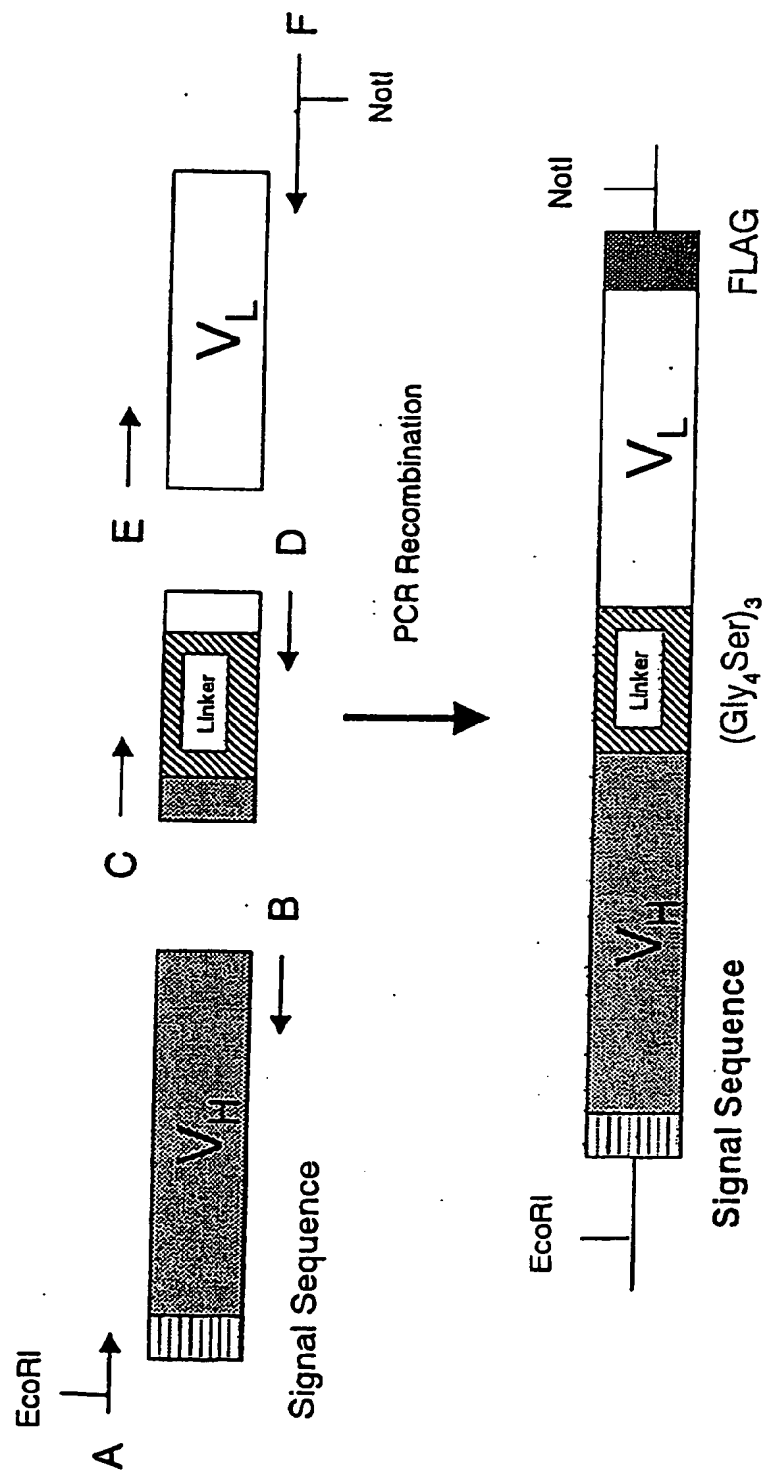


Fig. 48

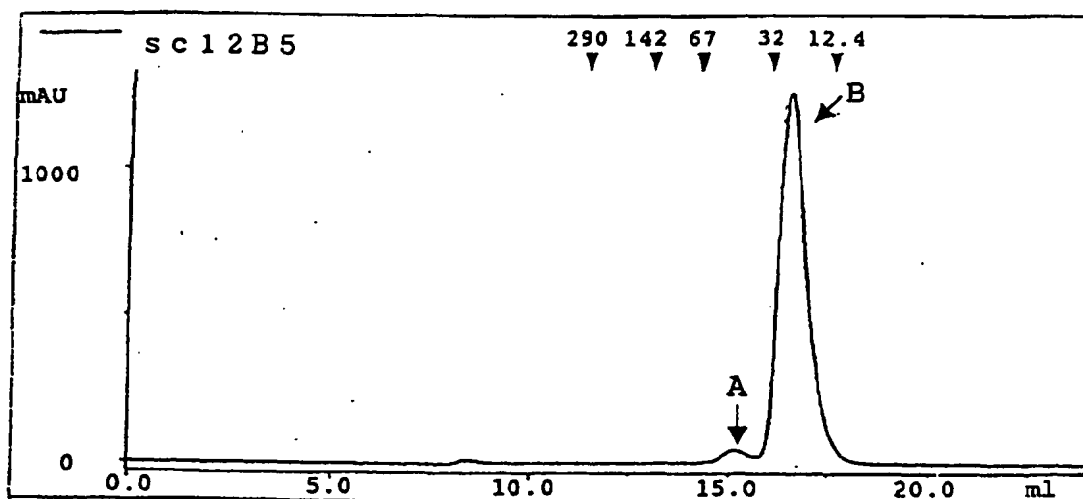


Fig. 49

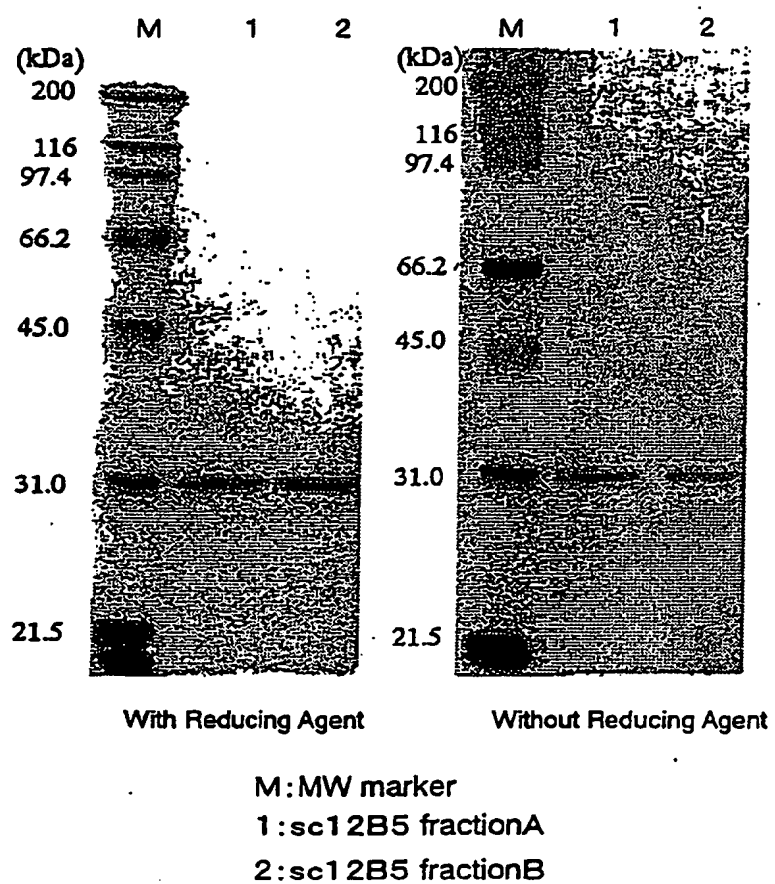


Fig. 50

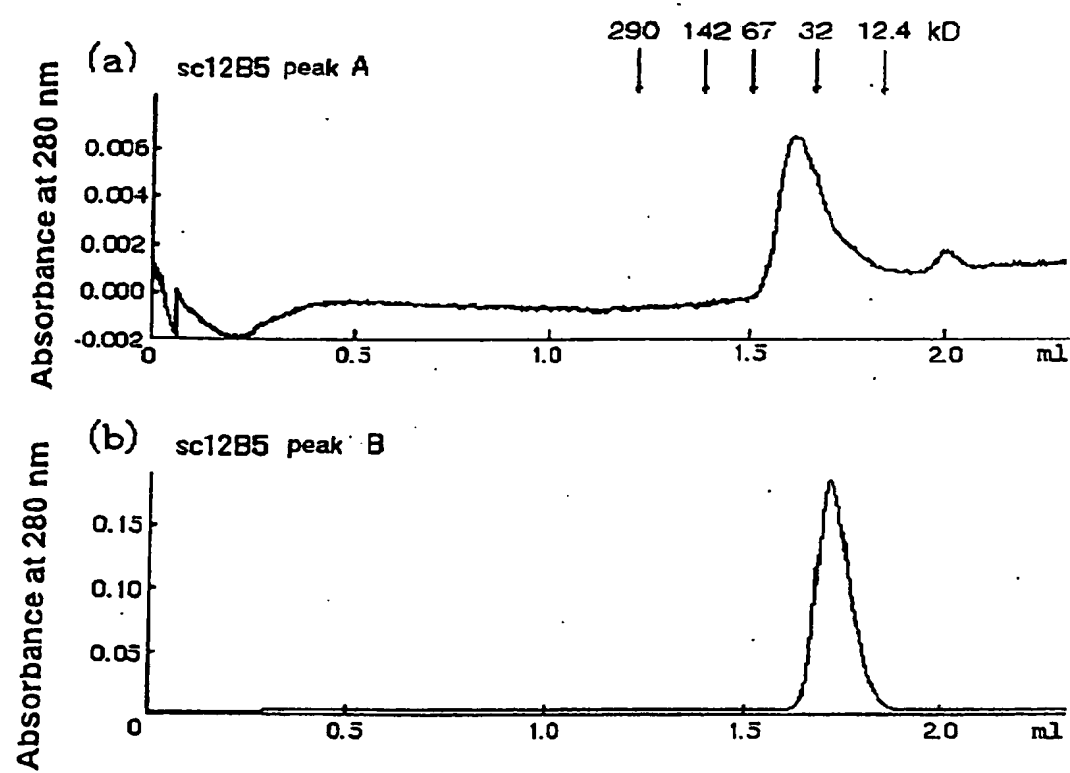


Fig. 51

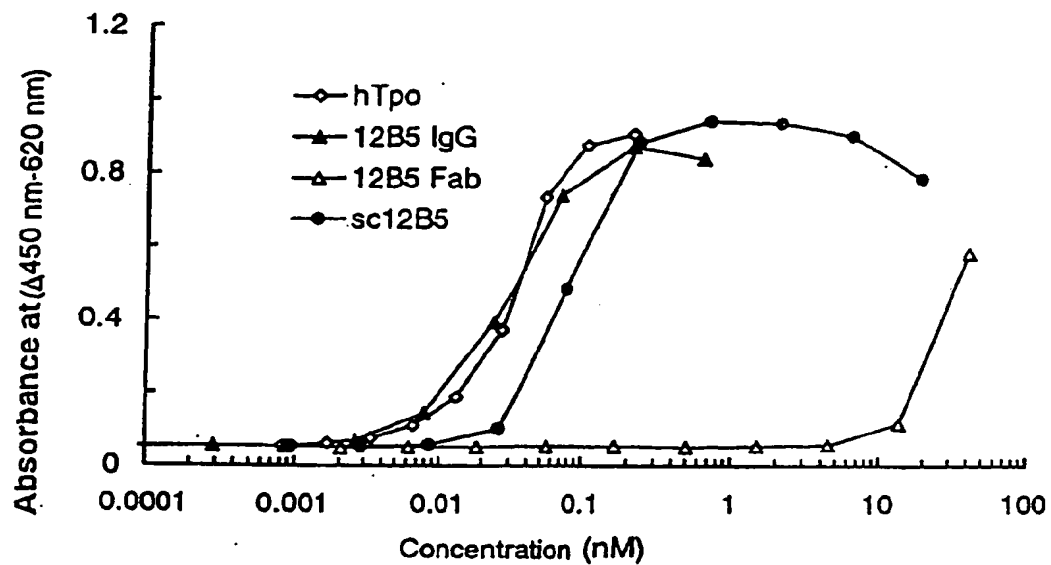


Fig. 52

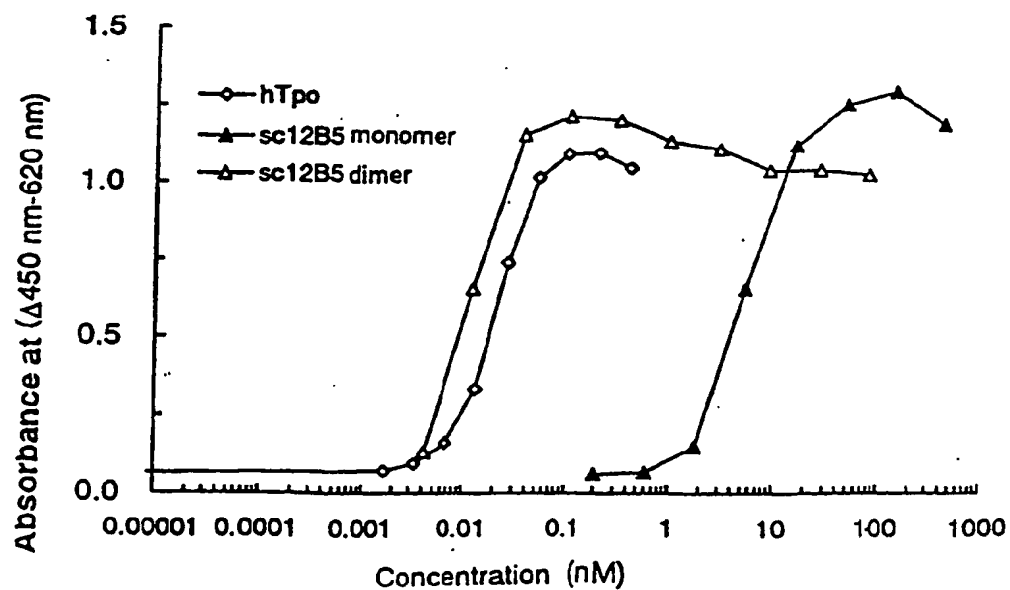


Fig. 53

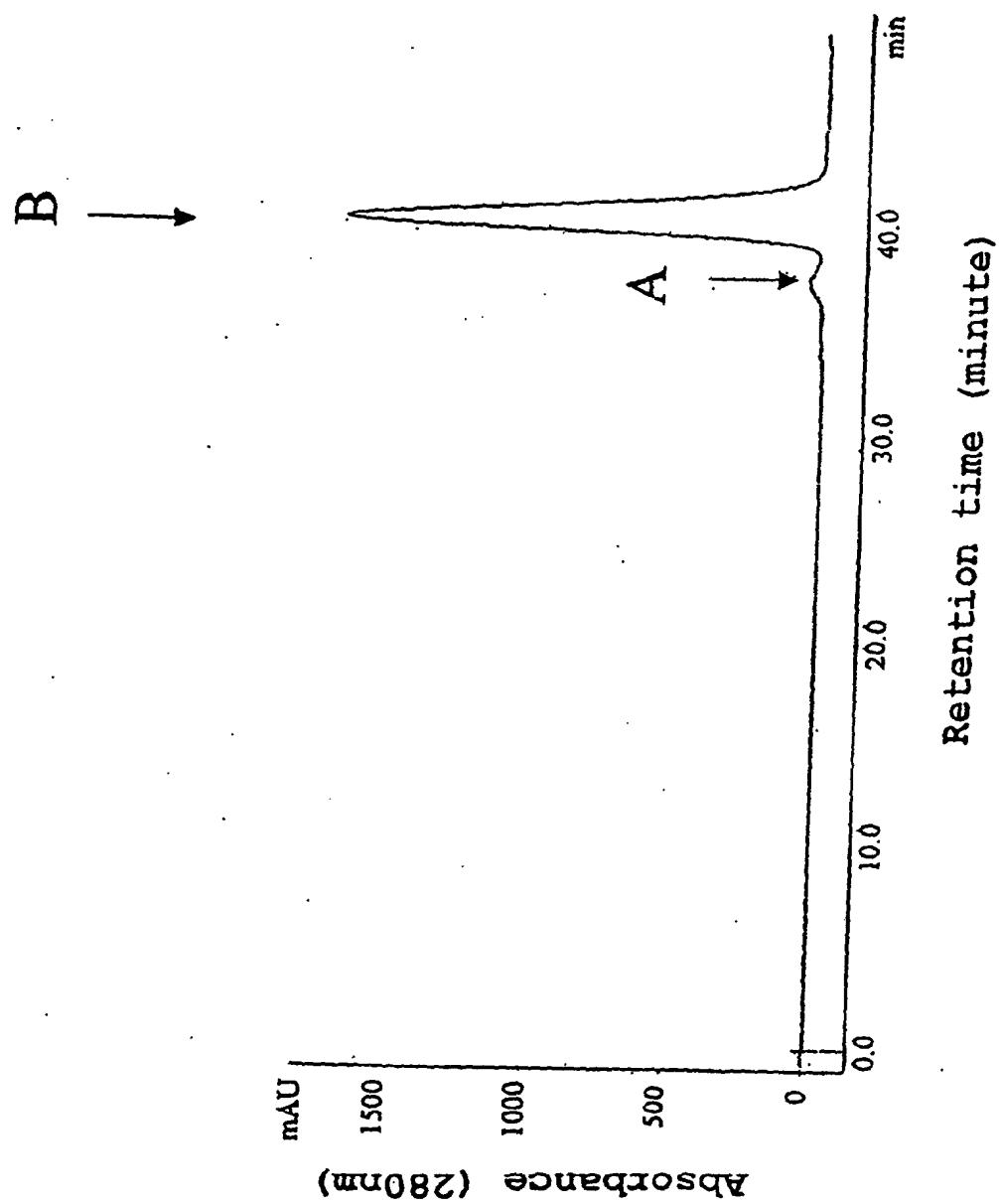




Fig. 54

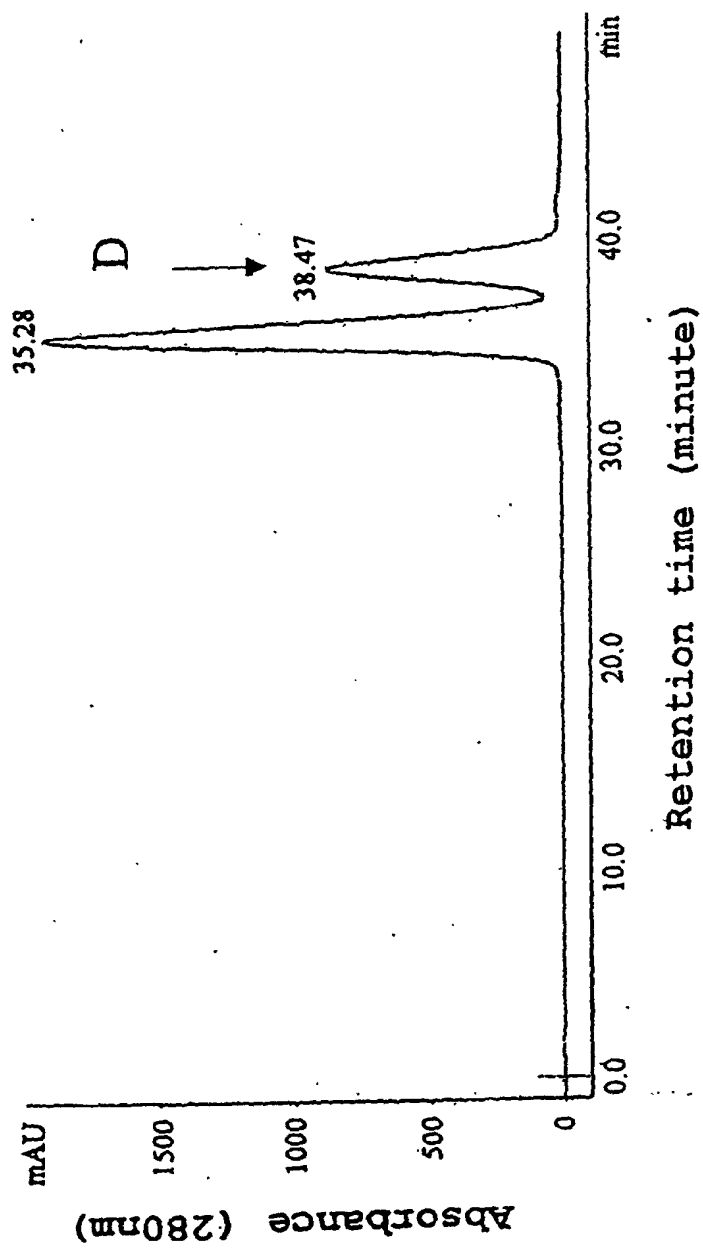


Fig. 5 5

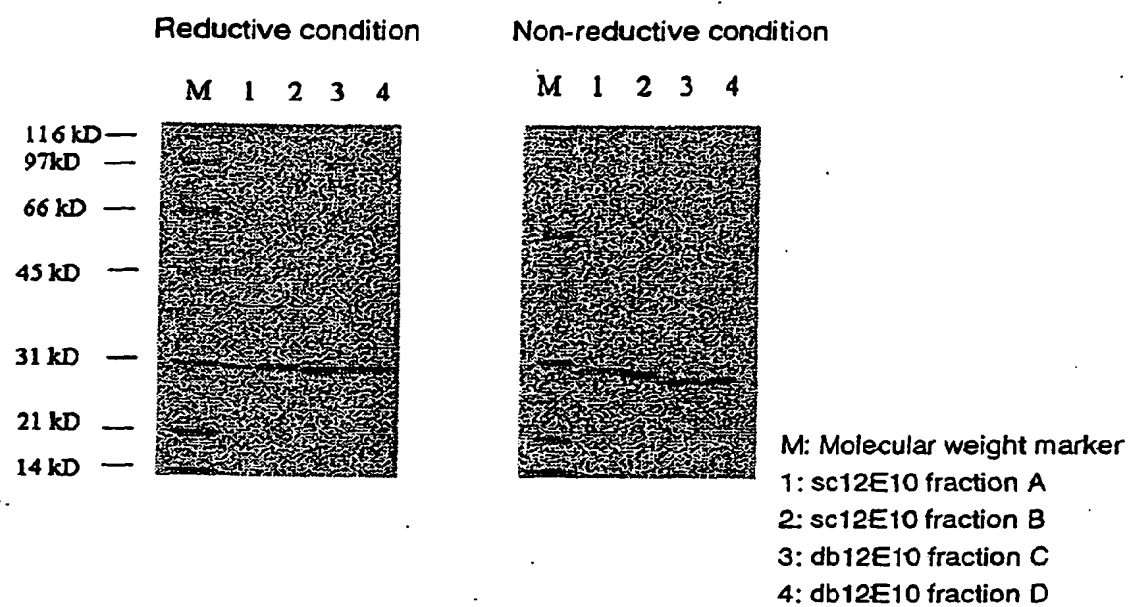


Fig. 56

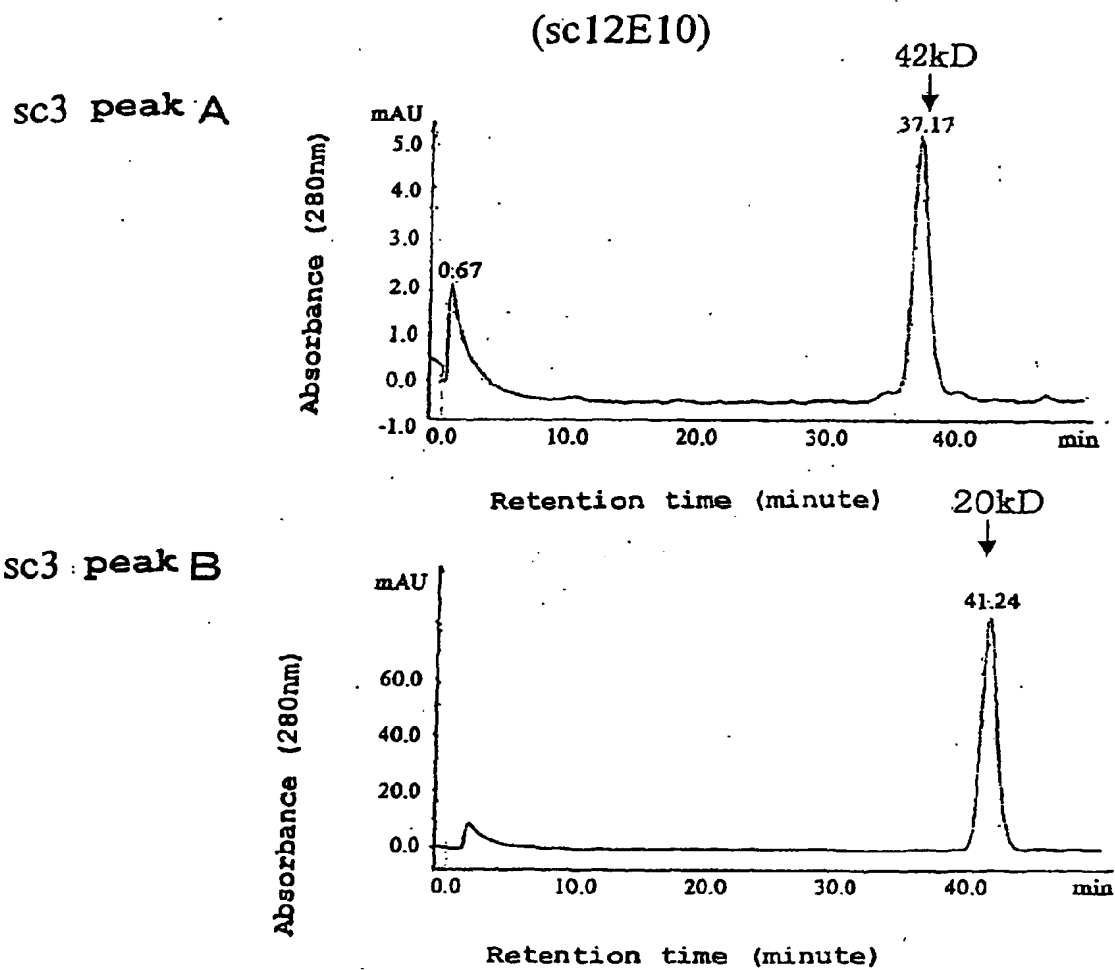


Fig. 57

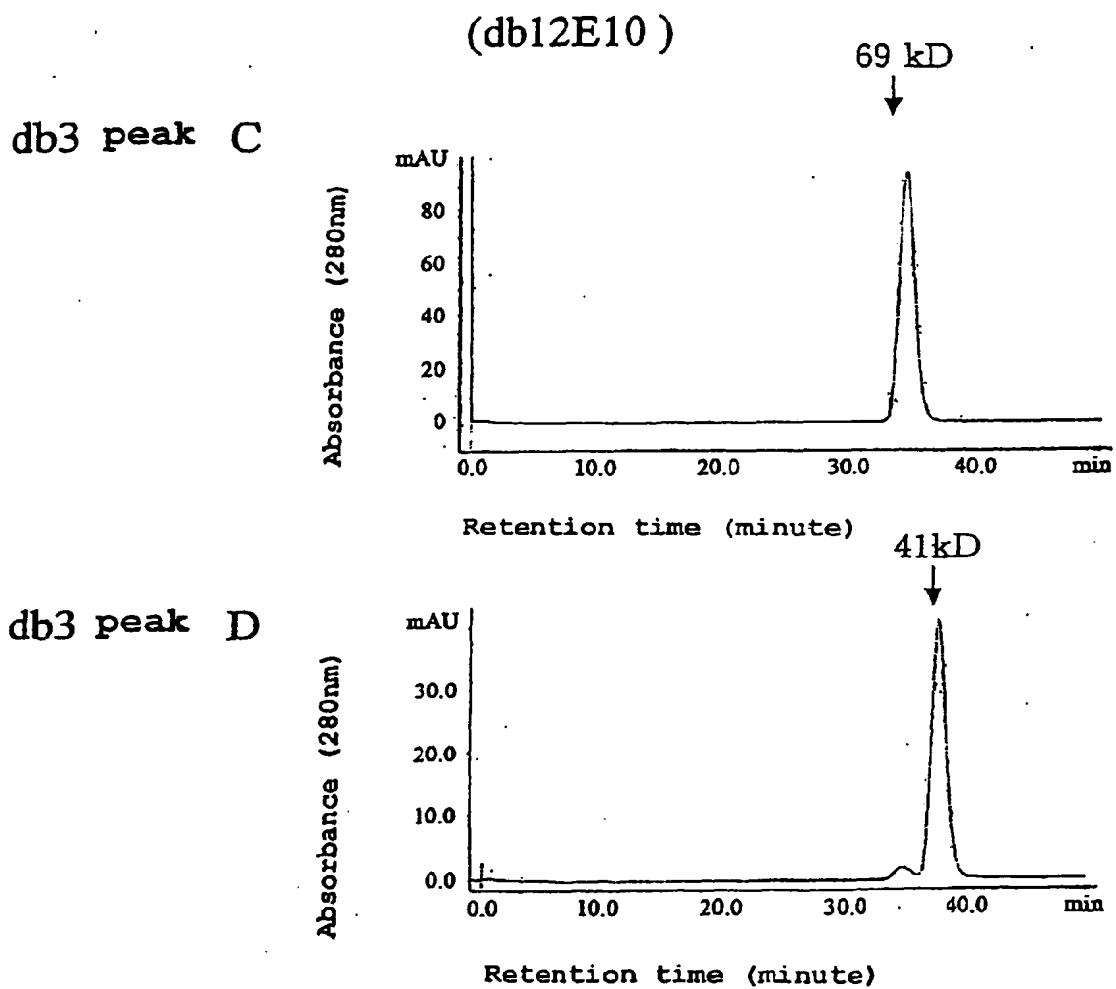


Fig. 5 8

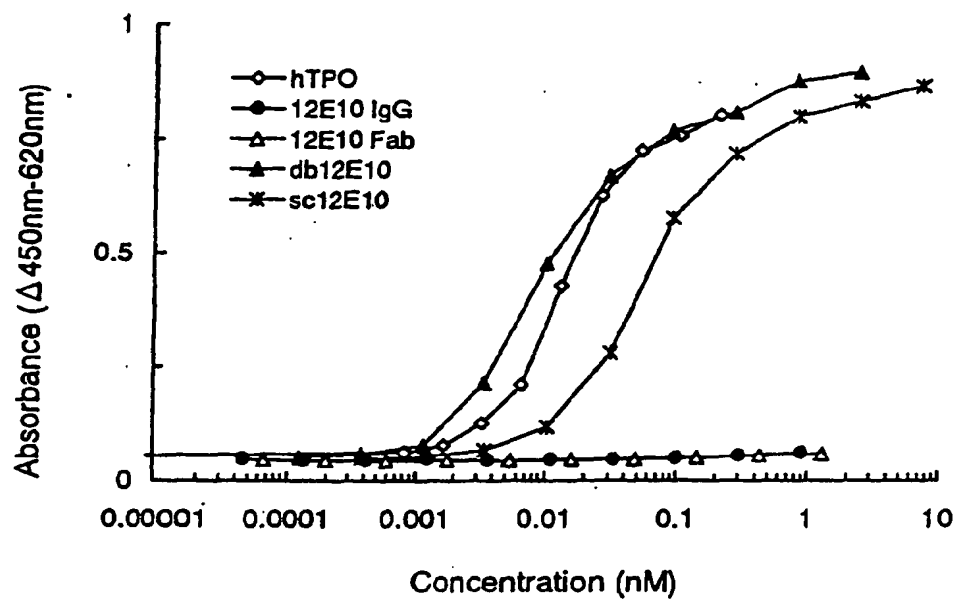
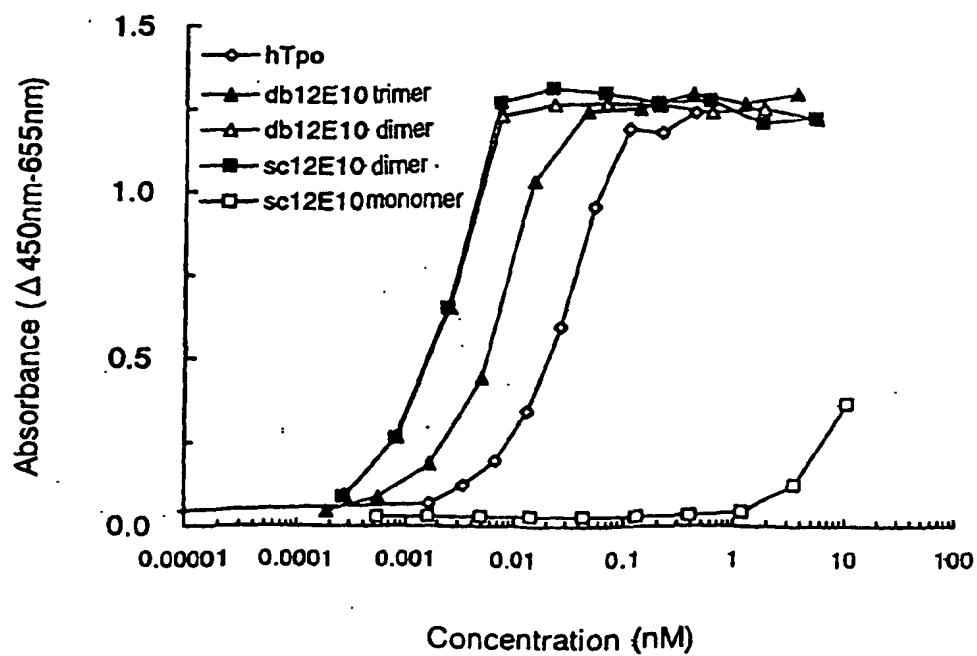


Fig. 5 9



## REFERENCES CITED IN THE DESCRIPTION

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## Patent documents cited in the description

- JP 2000095800 A [0004]
- WO 9910494 A [0004] [0033] [0053] [0244] [0249]
- JP 11063557 A [0048] [0180]
- WO 9219759 A [0060] [0068] [0107] [0126] [0233] [0258]
- WO 9413804 A [0064]
- JP 7236475 A [0168]
- JP 8255196 A [0233]
- JP 2000321821 A [0279]
- JP 1003288 W [0279]
- JP 2001277314 A [0279]

## Non-patent literature cited in the description

- M. SOUYRI et al. *Cell*, 1990, vol. 63, 1137 [0002]
- M. METHIA et al. *Blood*, 1993, vol. 82, 1395 [0002]
- F. DE SAUVAGE et al. *Nature*, 1994, vol. 369, 533 [0002]
- TD. BARTLEY et al. *Cell*, 1994, vol. 77, 1117 [0002]
- KIPRIYANOV et al. *Int. J. Cancer*, 1998, vol. 77, 9763-9772 [0003]
- XIE et al. *Nature Biotech.*, 1997, vol. 15, 768-771 [0004]
- KABAT, E.A. et al. Sequences of Protein of Immunological Interest. *Sequences of Protein of Immunological Interest*, 1983 [0045]
- *Protein Engineering*, 1996, vol. 9 (3), 299-305 [0050]
- SATO, K. et al. *Cancer Res.*, 1993, vol. 53, 1-6 [0062]
- MULLIGAN, R.C. et al. *Nature*, 1979, vol. 277, 108-114 [0069]
- MIZUSHIMA, S. et al. *Nucleic Acids Research*, 1990, vol. 18, 5322 [0069]
- *Bio/Technology*, 1991, vol. 9, 88-89 [0084] [0086] [0090]
- SAMBROOK et al. *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Laboratory Press, 1989 [0094]
- KABAT, E.A. et al. Sequences of Proteins of Immunological Interest. *Sequences of Proteins of Immunological Interest*, 1983 [0105]
- *J. Mol. Biol.*, 1987, vol. 196, 947-950 [0108]
- HOPP, T. P. et al. *Bio/Technology*, 1988, vol. 6, 1204-1210 [0121]
- HUSTON, J.S. et al. *Proc. Natl. Acad. Sci. USA*, 1988, vol. 85, 5879-5883 [0122]
- LEI, S.P. et al. *J. Bacteriology*, 1987, vol. 169, 4379-4383 [0125]
- *Nature*, 1988, vol. 322, 323-327 [0129]
- ZOKU-SEIKAGAKU JIKKEN KOZA. *Immuno-Biochemical Investigation*. Tokyo Kagaku Dojin [0172]
- *Eur. J. Immunol.*, 1996, vol. 26, 63-69 [0218]
- HOPP, T. P. et al. *Bio/Technology*, 1988, vol. 6, 1204-1210 [0229]
- OHTOMO et al. *Anticancer Res.*, 1998, vol. 18, 4311-4316 [0230]
- HUSTON et al. *Proc. Natl. Acad. Sci. USA*, 1988, vol. 85, 5879-5883 [0230]
- *Mol. Immunol.*, 1992, vol. 29, 1515-1518 [0249]